

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Run on: April 27, 2003, 16:51:16 ; Search time 9337 Seconds

Title: US-09-787-657-3

Sequence: 1 tactatagcgcgccgcaa.....aaaaaaaaaiaaaaaaaaaa 3770

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance; to have a

Result No.	Score	Query Match	Length	DB	ID	Description
1	3769.6	100.0	3770	6	AX098896	AX098896 Sequence
2	3769.6	100.0	3770	6	AX099316	AX099316 Sequence
3	3604.8	95.6	3590	6	AX427031	AX427031 Sequence
4	3394.2	90.0	3544	9	HSa272268	AJ272268 Homo sapi
5	3288.2	87.2	3464	9	HSa272213	AJ272213 Homo sapi
6	3229.6	85.7	3276	6	AX427033	AX427033 Sequence
7	3166.6	84.0	3213	6	AX098884	AX098884 Sequence
8	3166.6	84.0	3213	6	AX099304	AX099304 Sequence
9	3113.6	82.6	3114	6	AX098883	AX098883 Sequence
10	3113.6	82.6	3114	6	AX099303	AX099303 Sequence
11	3056.6	81.1	3057	6	AX098882	AX098882 Sequence
12	3056.6	81.1	3057	6	AX099302	AX099302 Sequence
13	2956.6	78.4	3710	10	MMU010949	AJ010949 Mus muscu
14	1211.6	32.1	3209	6	AX098926	AX098926 Sequence
15	1211.6	32.1	3209	6	AX099346	AX099346 Sequence
16	1197.4	31.8	3339	6	AX098927	AX098927 Sequence
17	1197.4	31.8	3339	6	AX099347	AX099347 Sequence
18	1139.6	30.2	3301	6	AX098925	AX098925 Sequence
19	1139.6	30.2	3301	6	AX099345	AX099345 Sequence
20	93.3	24.7	4125	6	AX302028	AX302028 Sequence
21	846.2	22.4	943	9	AB047621	AB047621 Macaca fa
22	446.8	11.9	175317	9	AC104298	AC104298 Homo sapi
23	434.8	11.5	183121	2	AC093417	AC093417 Homo sapi
24	415.2	11.0	154936	2	AC021252	AC021252 Homo sapi
25	415.2	11.0	186318	9	AC093205	AC093205 Homo sapi
26	293.4	7.8	1050	6	AX098690	AX098690 Homo sapi
27	293.4	7.8	1050	6	AX099310	AX099310 Sequence
28	286.4	7.6	162584	2	AC018594	AC018594 Homo sapi
29	275.6	7.3	2944	4	HSMB01956	AL137658 Homo sapi
30	248.6	6.6	969	6	AX098889	AX098889 Sequence
31	248.6	6.6	969	6	AX099309	AX099309 Sequence
32	238.2	6.3	390	11	G36524	G36524 SHIC-53209
33	238.2	6.3	155332	9	AC109581	AC109581 Homo sapi
34	238.2	6.3	181061	9	AC115282	AC115282 Homo sapi
35	235.6	6.2	912	6	AX098888	AX098888 Sequence
36	235.6	6.2	912	6	AX099308	AX099308 Sequence
37	224.6	6.0	163138	2	AC114521	AC114521 Rattus no
38	215.6	5.7	3432	9	HSR251367	AJ251367 Homo sapi
39	215.6	5.7	3433	9	HSR251368	AJ251368 Homo sapi
40	215.6	5.7	5303	9	AB011130	AB011130 Homo sapi
41	214	5.7	3186	6	AX098876	AX098876 Sequence
42	214	5.7	3186	6	AX099296	AX099296 Sequence
43	214	5.7	3248	6	AX098877	AX098877 Sequence
44	214	5.7	3248	6	AX099297	AX099297 Sequence
45	214	5.7	3327	6	AX098878	AX098878 Sequence

## ALIGNMENTS

RESULT	1
AX098896	
LOCUS	AX098896
DEFINITION	Sequence 21 from Patent WO0119870.
ACCESSION	AX098896
VERSION	AX098896.1 GI:13538125
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 3770)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
Brown, J. P. and Bertelme, P.		Secreoted soluble -g(a)2-g(d)-2, -g(a)2-g(d)-3 or -g(a)2-g(d)-4 calcium channel subunit polypeptides and screening assays using

same  
 JOURNAL Patent: WO 0119870-A 21 22-MAR-2001;  
 WARNER-LAMBERT COMPANY (US)  
 FEATURES Location/Qualifiers  
 source 1.3770  
 /Organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 1049 a 871 c 941 g 908 t 1 others  
 ORIGIN  
 Query Match 100.0%; Score 3769.6; DB 6; Length 3770;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTATAGGCGCGCGGAATTGCGACAGAGGGGGCGGAGCGGACAGGACAGGACCGCCG 60  
 DB 1 TACTATAGGCGCGCGCGGAATTGCGACAGAGGGGGCGGAGCGGAGCGGACAGGACCGCCG 60  
 QY 61 GCGCTGCCACCGCGCGCTCCGCGAGCTCCGCGCGCGCTCTCGTCCGCGCGCGAGC 120  
 DB 61 GCGCTGCCACCGCGCGCTCCGCGAGCTCCGCGCGCGCTCTCGTCCGCGCGCGAGC 120  
 QY 121 GGGCGGCTGGAGAGGAGCGGACAGCATGCGCGCGCGCTGCGCGCGCGCGCTCCGCGG 180  
 DB 121 GGGCGGCTGGAGAGGAGCGGACAGCATGCGCGCGCGCTGCGCGCGCGCGCTCCGCGG 180  
 QY 181 GGGCGCTGGCGCTTCTGCGCTGCGCGCGCTTCTACGCGCGCGCTGGGGAGCTGGTGGCT 240  
 DB 181 GGGCGCTGGCGCTTCTGCGCTGCGCGCGCTTCTACGCGCGCGCTGGGGAGCTGGTGGCT 240  
 QY 241 CGGAGCAGCAGATACCGCTCTCCGCTGTAAGCTCGGGCTCGCGCTTTGGTGGGAGCA 300  
 DB 241 CGGAGCAGCAGATACCGCTCTCCGCTGTAAGCTCGGGCTCGCGCTTTGGTGGGAGCA 300  
 QY 301 TAAATCCATGCTGTAGTACTCCGGTTCAGCTTTCGCAAAAGAAATACAAAGAGT 360  
 DB 301 TAAATCCATGCTGTAGTACTCCGGTTCAGCTTTCGCAAAAGAAATACAAAGAGT 360  
 QY 361 ATGAGAAAGACGTTGGCATAGAAAGAAATGATGGCTCCAAAGCTGTAAGAAAGCTGGCAA 420  
 DB 361 ATGAGAAAGACGTTGGCATAGAAAGAAATGATGGCTCCAAAGCTGTAAGAAAGCTGGCAA 420  
 QY 421 AGAACAATGGAAGATGTTTACAAAGAAAGCTGAGGCGCTGAGGCTGTTGAGAGCTG 480  
 DB 421 AGAACAATGGAAGATGTTTACAAAGAAAGCTGAGGCGCTGAGGCTGTTGAGAGCTG 480  
 QY 481 CAGAAGAACGACACCGTGAACATGATTTGATGACAGCTTACAGTATGATATCTTCAATG 540  
 DB 481 CAGAAGAACGACACCGTGAACATGATTTGATGACAGCTTACAGTATGATATCTTCAATG 540  
 QY 541 CTGTGCTGTAAATGAAAGGAGCAAAAGCGGGAATTTTGGAGCTGGGAAAGAAATGCA 600  
 DB 541 CTGTGCTGTAAATGAAAGGAGCAAAAGCGGGAATTTTGGAGCTGGGAAAGAAATGCA 600  
 QY 601 TCTTAGCCCCCAATGACATTTTAAATTTGCTGTGAACATCATGCTAGTGAAGTGCCTC 660  
 DB 601 TCTTAGCCCCCAATGACATTTTAAATTTGCTGTGAACATCATGCTAGTGAAGTGCCTC 660  
 QY 661 AAGTACCAAGCAATGTACAAAGAAAGCGCTGCAATTTGCAATGGGCTTATTGGTCTG 720  
 DB 661 AAGTACCAAGCAATGTACAAAGAAAGCGCTGCAATTTGCAATGGGCTTATTGGTCTG 720  
 QY 721 AATCTCTAAACAAAGTTTGTAGATTAATTTGACCGTGAACCTCTCTCATATGGCAGT 780  
 DB 721 AATCTCTAAACAAAGTTTGTAGATTAATTTGACCGTGAACCTCTCTCATATGGCAGT 780  
 QY 781 ACTTTGGAAGTGAAGGGCTTTTATAGAGTATCCGGGATTAATATGGAAACAGATG 840  
 DB 781 ACTTTGGAAGTGAAGGGCTTTTATAGAGTATCCGGGATTAATATGGAAACAGATG 840  
 QY 841 AGAATGGAAGTGAAGGGCTTTTATAGAGTATCCGGGATTAATATGGAAACAGATG 900  
 DB 841 AGAATGGAAGTGAAGGGCTTTTATAGAGTATCCGGGATTAATATGGAAACAGATG 900

QY 901 CTCGAAAGACGTGCTATTTTAACTGACGTGAGTGGCAGCATGAAGAGCTCCGTCTGA 960  
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 QY 961 CTATGGGAAGCAACGCTCATCCATTTTGGATTAACACTTTGGGATGATGACTTTTCA 1020  
 DB 961 CTATGGGAAGCAACGCTCATCCATTTTGGATTAACACTTTGGGATGATGACTTTTCA 1020  
 QY 1021 ACATTAATGCTTAAATGAGAGCTTCAATGATGAGAACTTGGCTGTAATGAACTTTG 1080  
 DB 1021 ACATTAATGCTTAAATGAGAGCTTCAATGATGAGAACTTGGCTGTAATGAACTTTG 1080  
 QY 1081 TCGAAGCCGACAGACCAAAAGAGCATTGAGGAGCATCTGGAACAACTTTTGCCA 1140  
 DB 1081 TCGAAGCCGACAGACCAAAAGAGCATTGAGGAGCATCTGGAACAACTTTTGCCA 1140  
 QY 1141 AAGGAATGGAATGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
 DB 1141 AAGGAATGGAATGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
 QY 1201 ACCACAGGAGCAAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
 DB 1201 ACCACAGGAGCAAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
 QY 1261 TGGACACTATGATATCAATCTTTGCAAAATACAAATGAGGAGATGAGGATGATGATGAT 1320  
 DB 1261 TGGACACTATGATATCAATCTTTGCAAAATACAAATGAGGAGATGAGGATGATGATGAT 1320  
 QY 1321 TGCATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 DB 1321 TGCATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 QY 1381 CCAACAAGGATTTTATACCAAGATCTCCAGCTTGGCTGATGATGATGATGATGATGATGAT 1440  
 DB 1381 CCAACAAGGATTTTATACCAAGATCTCCAGCTTGGCTGATGATGATGATGATGATGATGAT 1440  
 QY 1441 AATACCTTACGCTGCTTACCGCGCCCAAGATCATGACAGGAGATGATGATGATGATGAT 1500  
 DB 1441 AATACCTTACGCTGCTTACCGCGCCCAAGATCATGACAGGAGATGATGATGATGATGAT 1500  
 QY 1501 CGGAAGCTTACATTAACAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 DB 1501 CGGAAGCTTACATTAACAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 QY 1561 TAGCCATGCTGCTGTTTGTAGAGCAAGAAACAGATCGAAGGCACTTCTTGGGAG 1620  
 DB 1561 TAGCCATGCTGCTGTTTGTAGAGCAAGAAACAGATCGAAGGCACTTCTTGGGAG 1620  
 QY 1621 TGGTTGGCAGAGATGCTCCAGTGAAGAACTTGAAGAGCATCCCAATATCAAGTTAG 1680  
 DB 1621 TGGTTGGCAGAGATGCTCCAGTGAAGAACTTGAAGAGCATCCCAATATCAAGTTAG 1680  
 QY 1681 GGAATTCAGGTTATGCTTTCATATCAAAATATGATATATCTGACGATCCGGAAC 1740  
 DB 1681 GGAATTCAGGTTATGCTTTCATATCAAAATATGATATATCTGACGATCCGGAAC 1740  
 QY 1741 TCAGGCTGCTTACGAGAAAGAAAGGAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1800  
 DB 1741 TCAGGCTGCTTACGAGAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1800  
 QY 1801 TCTGTGAGAGTGGAGTGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
 DB 1801 TCTGTGAGAGTGGAGTGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
 QY 1861 AGAGGGGGAAGTTTTCATGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
 DB 1861 AGAGGGGGAAGTTTTCATGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
 QY 1921 TGAATGCAAAATGACTACTATTTATACAGACATCAAGGATGATGATGATGATGATGATGAT 1980  
 DB 1921 TGAATGCAAAATGACTACTATTTATACAGACATCAAGGATGATGATGATGATGATGATGAT 1980

QY	1981	GCCCTTCCAGAGGATCATGGGAAATATTTCTCCGAGGAAATGAACATTCGAAGAAGGCC	2040
Db	1981	GCCTTCCAGAGGATCATGGGAAATATTTCTCCGAGGAAATGAACATTCGAAGAAGGCC	2040
QY	2041	TGCATGACTTTGGAACATCCCGATGTGCTCTGGCAATATAATGTCTCTA:TCGACACTG	2100
Db	2041	TGCATGACTTTGGAACATCCCGATGTGCTCTGGCAATATAATGTCTCTA:TCGACACTG	2100
QY	2101	ACCTACACCTTGAGCACCCGCCATCTGTCTCAGTTAGAACGATTAAGCTTTACCTTAAAG	2160
Db	2101	ACCTACACCTTGAGCACCCGCCATCTGTCTCAGTTAGAACGATTAAGCTTTACCTTAAAG	2160
QY	2161	GCAAGAAGCCCTCCTCCAGTGTGATTAAGTAATGATTCAGAAAGCTCTTTTGTACGGGG	2220
Db	2161	GCAAGAAGCCCTCCTCCAGTGTGATTAAGTAATGATTCAGAAAGCTCTTTTGTACGGGG	2220
QY	2221	TGTGTAGTGGCCCATTTGAAGCGATTTGTGACACAGCCGTGGCCCTCAACAAATTCGAAATTT	2280
Db	2221	TGTGTAGTGGCCCATTTGAAGCGATTTGTGACACAGCCGTGGCCCTCAACAAATTCGAAATTT	2280
QY	2281	CTGACAAAGGCGGTGAGAGTTGCTCTCTGGGCACTTCGACAGGGGCGCTTC:AGAAATCAAC	2340
Db	2281	CTGACAAAGGCGGTGAGAGTTGCTCTCTGGGCACTTCGACAGGGGCGCTTC:AGAAATCAAC	2340
QY	2341	TGTTTGTGCGGGGCGTACACACTACCAATTCAGAGACTTCTGTAAAGCTGG:GACAAAGAGA	2400
Db	2341	TGTTTGTGCGGGGCGTACACACTACCAATTCAGAGACTTCTGTAAAGCTGG:GACAAAGAGA	2400
QY	2401	ACATTTTAAAGCAGACACTTTTCCCTCTGTGGTACCGAAGACCGCTGAG:GACAAATCCAG	2460
Db	2401	ACATTTTAAAGCAGACACTTTTCCCTCTGTGGTACCGAAGACCGCTGAG:GACAAATCCAG	2460
QY	2461	GGAGCTTCGTCTACTCGATCCCATTCAGACACTGGACACTCAATTAAG:TAATGTGTGA	2520
Db	2461	GGAGCTTCGTCTACTCGATCCCATTCAGACACTGGACACTCAATTAAG:TAATGTGTGA	2520
QY	2521	CAGAGAGACATCCATCCACTCTCTGGATGAAGCGAAATCTCTGTGTGGAGCTGTAG	2580
Db	2521	CAGAGAGACATCCATCCACTCTCTGGATGAAGCGAAATCTCTGTGTGGAGCTGTAG	2580
QY	2581	GCATTCAGATGAACCTTAATTTTCCAAAGGAAGTTCGTGGAGCTGCCAG:TAGACAGTGTG	2640
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QY	2641	CTTCCCTGGATGGCAAAATGCTCCATCAGCTGTGATGATGAGAGCTGTGAATTTGTACTCA	2700
Db	2641	CTTCCCTGGATGGCAAAATGCTCCATCAGCTGTGATGATGAGAGCTGTGAATTTGTACTCA	2700
QY	2701	TAGACATTAATGATTTATTTTGTGTCTGTAAGACTACACACAGACTGGAGACTTTTTTG	2760
Db	2701	TAGACATTAATGATTTATTTTGTGTCTGTAAGACTACACACAGACTGGAGACTTTTTTG	2760
QY	2761	GTCGATATCGAGGAGCTGTGATGAACAAATTTCTTAACAATGGGCCCTTTAAAGAAATTA	2820
Db	2761	GTCGATATCGAGGAGCTGTGATGAACAAATTTCTTAACAATGGGCCCTTTAAAGAAATTA	2820
QY	2821	CCCTTTATGACTACCAAGGCATGTGTAGAGCCACAAAGAAAGCAGGAGTGGCCCATG	2880
Db	2821	CCCTTTATGACTACCAAGGCATGTGTAGAGCCACAAAGAAAGCAGGAGTGGCCCATG	2880
QY	2881	GCCCTCCGGATCTTTTAATGATGCTCTCTCTGTGCAAGTAAATTGATCATAT:ACAGAACTTG	2940
Db	2881	GCCCTCCGGATCTTTTAATGATGCTCTCTCTGTGCAAGTAAATTGATCATAT:ACAGAACTTG	2940
QY	2941	TCTTGTTCCTGTGTGAATTAACCTCTGCAAGTGTGTGGCACTCCGATTAATACAGCTTAAG	3000
Db	2941	TCTTGTTCCTGTGTGAATTAACCTCTGCAAGTGTGTGGCACTCCGATTAATACAGCTTAAG	3000
QY	3001	CCGAGAAATTTGAAACAGACCTGTGAAGCTTTGTGATATCAATATTCACAG:ATTCGCTCTG	3060
Db	3001	CCGAGAAATTTGAAACAGACCTGTGAAGCTTTGTGATATCAATATTCACAG:ATTCGCTCTG	3060
QY	3061	AGCGCAACATCAAGGAGACTACAGGAAATTTGCTTTGGAAGACTGCTC:AACTCCTTTG	3120

Db	3061	AGGGCACCATCAAGGAGACTACAGGGAAATATGCTTGTAAAGCTCTCCAAATCTCTTG	3120
Qy	3121	TCATCAGACAATCCCAACAGACAACTCTTCATGCTGGTGGAGACAGCTGCCTC	3180
Db	3121	TCATCAGACAATCCCAACAGACAACTCTTCATGCTGGTGGAGACAGCTGCCTC	3180
Qy	3181	GTGAATCTGTGGCCCCCATCACATGGACCCATTGAAATCAGGTAAATGAAATCCCTTA	3240
Db	3181	GTGAATCTGTGGCCCCCATCACATGGACCCATTGAAATCAGGTAAATGAAATCCCTTA	3240
Qy	3241	AGGTGAACGTCTAAAGGCCCAAGATCAGAAAGGCCCAAGATCTGTCAATGGCTTCC	3300
Db	3241	AGGTGAACGTCTAAAGGCCCAAGATCAGAAAGGCCCAAGATCTGTCAATGGCTTCC	3300
Qy	3301	ATCCTGAGAGAAATGCACAGGAGTGTGGGGGTGGCGCGATGCTCCAAAGCCACAGACTCC	3360
Db	3301	ATCCTGAGAGAAATGCACAGGAGTGTGGGGGTGGCGCGATGCTCCAAAGCCACAGACTCC	3360
Qy	3361	TCCCTTCTGCTCCCTGCTTGTGATGCTTTCTCAAGGTGACACTGAGATGTTCTC	3420
Db	3361	TCCCTTCTGCTCCCTGCTTGTGATGCTTTCTCAAGGTGACACTGAGATGTTCTC	3420
Qy	3421	TTACGACACTGAGATGTTCTCTGGCATGCTGAATCATGATTAACCTGTAACCAAAATAT	3480
Db	3421	TTACGACACTGAGATGTTCTCTGGCATGCTGAATCATGATTAACCTGTAACCAAAATAT	3480
Qy	3481	GGTGCACATACGAGACATGAATATATGCCAACCATCAGCATCTCATCATGATTTTAAAC	3540
Db	3481	GGTGCACATACGAGACATGAATATATGCCAACCATCAGCATCTCATCATGATTTTAAAC	3540
Qy	3541	TGTGGTGATATAAACTCTTAAAGATATGTGTACAAAAAGTATATCATCTTTTACT	3600
Db	3541	TGTGGTGATATAAACTCTTAAAGATATGTGTACAAAAAGTATATCATCTTTTACT	3600
Qy	3601	TTGGCAGTCATCAAAATGTGAGTTCGCCACATGATTAATCACCTTCATCAGAAATGGAC	3660
Db	3601	TTGGCAGTCATCAAAATGTGAGTTCGCCACATGATTAATCACCTTCATCAGAAATGGAC	3660
Qy	3661	CGCAAGTGGTAGCGAGTGTCCCTTCTGCTTGAACCTATTGAACCAATTTAAACTGTG	3720
Db	3661	CGCAAGTGGTAGCGAGTGTCCCTTCTGCTTGAACCTATTGAACCAATTTAAACTGTG	3720
Qy	3721	TACTTTTAAATAAAGTATATTAATATCATTAATAAAAAAAAAAAAAAAAAAAAAA	3770
Db	3721	TACTTTTAAATAAAGTATATTAATATCATTAATAAAAAAAAAAAAAAAAAAAAAA	3770

[illegible]

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	TACTATATAGGGCGGCGCGGAATTCGGACAGAGCGGCGGCGAGCGAGCGAGCGAGCCCGC	60
Db	1	TACTATATAGGGCGGCGCGCGGAATTCGGACAGAGCGGCGGCGAGCGAGCGAGCGAGCCCGC	60
Oy	61	GGCGTGGCCCCACCGGGCGGTCCGGCGAGTCCCGCGGCGCGCTCTCGTCCGCCGCGAGC	120
Db	61	GGCGTGGCCCCACCGGGCGGTCCGGCGAGTCCCGCGGCGCGCTCTCGTCCGCCGCGAGC	120
Oy	121	GGGCGGCGTGGAGGAGGAGCCACAGTATGGCCGGGCGGGCTCCGCGCGCGCGCGTCCGGG	180
Db	121	GGGCGGCGTGGAGGAGGAGCCACAGTATGGCCGGGCGGGCTCCGCGCGCGCGCGTCCGGG	180
Oy	181	GGGCGTCCGGCGCTTCTCGCTGCCGCGCTTCTTCACGCCGCGCTGGGGACGTGGTGGCT	240
Db	181	GGGCGTCCGGCGCTTCTCGCTGCCGCGCTTCTTCACGCCGCGCTGGGGACGTGGTGGCT	240
Oy	241	CGGAGGAGAGATACCGCGTCCCGTGGTGAAGCTCTGGGCGCTGGGCTTTTGTGGGAGAG	300
Db	241	CGGAGGAGAGATACCGCGTCCCGTGGTGAAGCTCTGGGCGCTGGGCTTTTGTGGGAGAG	300
Oy	301	TAAATTCATTGCTGCTAAGTACTTCGGTCCGACGCTTCTGCAGAAAGAAATACAAAGAT	360
Db	301	TAAATTCATTGCTGCTAAGTACTTCGGTCCGACGCTTCTGCAGAAAGAAATACAAAGAT	360
Oy	361	ATGAGAGAAACGCTTGCCATAGAGAAATTTGATGGCTCCAACTGCTGTAAAGAGCTGGCA	420
Db	361	ATGAGAGAAACGCTTGCCATAGAGAAATTTGATGGCTCCCAACTGCTGTAAAGAGCTGGCA	420
Oy	421	AGAACATGAGAGATGTTTTCACAAGAGTGTGAGGCGTGCAGCGCTGTGGTAGAGCTG	480
Db	421	AGAACATGAGAGATGTTTTCACAAGAGTGTGAGGCGTGCAGCGCTGTGGTAGAGCTG	480
Oy	481	CAGAGAGACACACTTGAACATGATTTGATGACAGCTTACAGATGATTACTTCAATG	540
Db	481	CAGAGAGAGCACCTGTGAACATGATTTGATGACAGCTTACAGATGATTACTTCAATG	540
Oy	541	CTGTGCTGTAATTAATGAAGGAGCAAAAGCGGAAATTTTGGAGCTGGGAAGCAATTTCA	600
Db	541	CTGTGCTGTAATTAATGAAGGAGCAAAAGCGGAAATTTTGGAGCTGGGAAGCAATTTCA	600
Oy	601	TCTTAGCCCCAATGACATTTTAATTAATTTGGCTGTGAACATCAGCTTAAGTGAAGTCC	660
Db	601	TCTTAGCCCCAATGACATTTTAATTAATTTGGCTGTGAACATCAGCTTAAGTGAAGTCC	660
Oy	661	AGTCCCAACAGACATGTACAAACAAGACCTTGCATTTGTCAATGGGGTTTATTGGTCTG	720
Db	661	AGTCCCAACAGACATGTACAAACAAGACCTTGCATTTGTCAATGGGGTTTATTGGTCTG	720
Oy	721	AATCTCTAAACAAGTTTGTGTAGATTAACCTTGACCGTACCCATCTCTCATATGGCAGT	780
Db	721	AATCTCTAAACAAGTTTGTGTAGATTAACCTTGACCGTACCCATCTCTCATATGGCAGT	780
Oy	781	ACTTTGGAAGTGCAAAGGGCTTTTATAGCAGATATCCGGGGATTAAATGGAGCAAGATG	840
Db	781	ACTTTGGAAGTGCAAAGGGCTTTTATAGCAGATATCCGGGGATTAAATGGAGCAAGATG	840
Oy	841	AGAATGGAGTATGGCTTGGACTGCAGAGAACCGAAATGTGATCATCCAGGACGACACTT	900
Db	841	AGAATGGAGTATGGCTTGGACTGCAGAGAACCGAAATGTGATCATCCAGGACGACACTT	900
Oy	901	CTCCGAAAGAGCTGTGCTATTATTAGTTAGCTGACGTGAGTGCAGATGAAAGAGACTCGCTG	960
Db	901	CTCCGAAAGAGCTGTGCTATTATTAGTTAGCTGACGTGAGTGCAGATGAAAGAGACTCGCTG	960
Oy	961	CTATCGGAGAGCAACAGTCTATCCATTTTGGATATACATTGGGATGATCATTCTTCA	1020
Db	961	CTATCGGAGAGCAACAGTCTATCCATTTTGGATATACATTGGGATGATCATTCTTCA	1020
Oy	1021	ACATTAATGCTTATATAGGAGGCTTCACTATGTGAACTTGGCTGATGAACTTTGG	1080
Db	1021	ACATTAATGCTTATATAGGAGGCTTCACTATGTGAACTTGGCTGATGAACTTTGG	1080

Db	1021	ACATAATTGCTTATATATGAGAGCTTCACTATGTGGAACTTGCCTGTAATGGAACTTTGG	1080
Qy	1081	TGCAAGCCGACAGAGCAAAACAAGAGACCTTCAGGAGACATCTGGACAACACTTTTCGGCA	1140
Db	1081	TGCAAGCCGACAGAGCAAAACAAGAGACCTTCAGGAGACATCTGGACAACACTTTTCGGCA	1144
Qy	1141	AAGGAATTGGAAATGTTGGATATAGCTCTGGAATGAGGCCCTTCAACATTTCTGACTGATTTCA	1200
Db	1141	AAGGAATTGGAAATGTTGGATATAGCTCTGGAATGAGGCCCTTCAACATTTCTGACTGATTTCA	1200
Qy	1201	ACCACACGGGACAAGGAAGTATCTGCAGTCAGGCCCATATGCTCTAACTGATGGGGCGG	1260
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Qy	1261	TGGACACCTATGATACAAATCTTTGCAAAATACAAATTGGCCAGATGGAAGGTTGGCACT	1320
Db	1261	TGGACACCTATGATACAAATCTTTGCAAAATACAAATTGGCCAGATGGAAGGTTGGCACT	1320
Qy	1321	TCACATACCTCATTTGGAGAGAGGCTGGCTTTCAGACAAATCTAAAGTGATGGGCTGTG	1380
Db	1321	TCACATACCTCATTTGGAGAGAGGCTGGCTTTCAGACAAATCTAAAGTGATGGGCTGTG	1380
Qy	1381	CCAAACAAAGATTTTTTACCAGATCTCCACCTTGGCTGATGTGACAGAGAATGTCAATGG	1440
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Qy	1441	AATACCTTACAGTGTGTCGCGGCCCAAAAGTCATCGACACAGAGACATGATGGGTGCGA	1500
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Qy	1861	AGACGGGGAAGTTTTCATGAGAGTGAAGAAGACAGTGGCAAAAGGAAACGGGTTTTGG	1920
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Db	1921	TGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTTTCAGTTTAGTGTGG	1980
Qy	1981	CGTTTTCAGAGGTCATTTGGGAAATATTTCTTCGAGGGGATGTAACTATCGAAGAGGCC	2040
Db	1981	CGTTTTCAGAGGTCATTTGGGAAATATTTCTTCGAGGGGATGTAACTATCGAAGAGGCC	2040
Qy	2041	TGCATGACTTAAACAATCCCGATGTGTCTTGGCAGATGAATAGTGTCTTACTGCAACACG	2100
Db	2041	TGCATGACTTAAACAATCCCGATGTGTCTTGGCAGATGAATAGTGTCTTACTGCAACACG	2100
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Db	1723	TGGTGATGACAATGACTACTATTATATACAGACATCAAGGCTACTCTTTCAGTTTACGTG	1782
Qy	1978	TGGCGCTTTCCAGAGGTCATGAGAAATATTTCTTCCGAGGGAATGTAAACCATCGAAGAG	2037
Db	1783	TGGCGCTTTCCAGAGGCTCATGAGAAATATTTCTTCCGAGGGAATGTAAACCATCGAAGAG	1842
Qy	2038	GGCTGCATGACTTAAAGAACTCCCGATGTGTCTTTGGCAGATGAATGTGTCCTACTGCACA	2097
Db	1843	GGCTGCATGACTTAAAGAACTCCCGATGTGTCTTGGCAGATGAATGTGTCCTACTGCACA	1902
Qy	2098	CTGACCTACACCTGTGAGACACCGGCATGTGTCTGATAGTAAGGATTAACCTCACTAA	2157
Db	1903	CTGACCTACACCTGTGAGACACCGGCATGTGTCTGATAGTAAGGATTAACCTCACTAA	1962
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Qy	2338	ACCTGTTTGTCCGGGCTGAGACACTCACCAATAGAGACTTCTGAAAGCTGGGCGACAGG	2397
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Db	2203	AGAACTTTTAAACGACAGACCATTTCCCTCTCTGTGATCCGAAAGCCGCTGACACAGATTTC	2262
Qy	2458	CAGGGGCTTCGCTCTCTGATGCCATTCATGACACTGGACACGTCAATTAAGCAATGTGG	2517
Db	2263	CAGGGGCTTCGCTCTCTGATGCCATTCATGACACTGGACACGTCAATTAAGCAATGTGG	2322
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Qy	2938	TTTGTCTTCTCCGTGTGGAATTTAACTCTGTGAGTGTGGGCACTCCGATATGACAGCTA	2997
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Db	2803	AAGCCAGAATAATTGAACAGACCCTGGAGCCTTGATGTAAGTATTCAGACTTCGTCT	2862
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LOCUS			
DEFINITION	HSA272213	3464 bp mRNA linear PRI 20-MAR-2001	
		Homo sapiens mRNA for calcium channel alpha2-delta3 subunit (splice variant).	
ACCESSION	AJ272213		
VERSION	AJ272213.1	GI:7024360	
KEYWORDS		calcium channel alpha2-delta3 subunit.	
SOURCE		human.	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE			
AUTHORS		1 (bases 1 to 3464)	
TITLE		Hanke,S., Bugert,P., Chudek,J. and Kovacs,G.	
		Cloning a calcium channel alpha2delta-3 subunit gene from a	
		putative tumor suppressor gene region at chromosome 3p21.1 in	
		conventional renal cell carcinoma	
JOURNAL		Gene 264 (1), 69-75 (2001)	
MEDLINE		21142395	
PUBMED		11245980	
REFERENCE		2. (bases 1 to 3464)	
AUTHORS		Kovacs,G.	

TITLE Direct Submission  
JOURNAL Submitted (17-FEB-2000) Kovacs G., Department of Urology,  
University of Heidelberg, Laboratory of Molecular Oncology, Im  
Neuenheimer Feld 365, Heidelberg, 69120, GERMANY

FEATURES  
Source Location/Qualifiers

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PRECHRRRPA"

CDS

BASE COUNT 1003 a 762 c 834 g 865 t  
ORIGIN

Query Match 87.2%; Score 3288.2; DB 9; Length 3464;  
Best Local Similarity 97.2%; Pred. No. 0;

Matches 3412; Conservative 1; Mismatches 9; Indels 89; Gaps 3;

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DB 43 CTCCTCTGAGGTGAGAGCTCTGGGCGCTCTTTGGTGGGAGATAAATCCATTGCTG 315  
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DB 103 CTAGTACTCCGGTCCACCTCTCTCAAAAGAAATCAAAAGATGAGAAAGCTTG 375  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 REFERENCE  
 AUTHORS Curtis, R.A.  
 TITLE 21784, a human calcium channel family member and uses thereof  
 JOURNAL Patent: WO 0194584-A 3 13-DEC-2001.  
 Millennium Pharmaceuticals, Inc. (US)  
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ACCESSION	AX098884		PAT 02-APR-2001
VERSION	AX098884.1	GI:13538120	
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SOURCE	human.		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 3213)		
	Brown,J.P. and Bertelli,F.		
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JOURNAL	Patent: WO 0119870-A 9 22-MAR-2001;		
FEATURES	WARNER-LAMBERT COMPANY (US)		
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Matches 3195; Conservative	0; Mismatches 0; Indels 18; Gaps 1;		
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REFERENCE 1 (bases 1 to 3114)  
 AUTHORS Brown, J.P. and Bertelli, F.  
 TITLE Secreted soluble -g(a)2-g(d)-2, -g(a)2-g(d)-3 cr -g(a)2-g(d)-4  
 calcium channel subunit polypeptides and screening assays using  
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 JOURNAL Patent: WO 0119870-A 8 22-MAR-2001;  
 WARNER-LAMBERT COMPANY (US)  
 FEATURES Location/Qualifiers  
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 DB 1081 TGCAGTCAGGCGCATGCTCATTAATGATGGGCGGTGACACCTATGATACATCTTT 1140  
 OY 1284 GCATAATTAATTTGGCAATGCAAAAGTTTGCATCTTCAATACCTCATTTGACAGAG 1343  
 DB 1141 GCATAATTAATTTGGCAATGCAAAAGTTTGCATCTTCAATACCTCATTTGACAGAG 1200  
 OY 1344 GCTGCGTTTGACAGACATCTAAAGTGATGGGCGGTGACACAAAGAAATTTTACCAG 1403  
 DB 1201 GCTGCGTTTGACAGACATCTAAAGTGATGGGCGGTGACACAAAGAAATTTTACCAG 1260  
 OY 1404 ATCTCCACCTTGGCTGATGTGACAGAGAAATGTCATGAAATACCTTCACGTCTTACC 1463  
 DB 1261 ATCTCCACCTTGGCTGATGTGACAGAGAAATGTCATGAAATACCTTCACGTCTTACC 1320  
 OY 1464 CCCAAGTATGACAGCAGAGATGATGTGTGTGACCCGAAGCTTACATTTGACAGACT 1523  
 DB 1321 CCCAAGTATGACAGCAGAGATGATGTGTGTGACCCGAAGCTTACATTTGACAGACT 1380  
 OY 1524 CTGACGTATGATCAGAGGCGCCGCTGATGACACATCTGACCTGCTGTTTATAGTA 1583  
 DB 1381 CTGACGTATGATCAGAGGCGCCGCTGATGACACATCTGACCTGCTGTTTATAGTA 1440  
 OY 1584 CAGAACGAAACAGATCGAAGGGCATTTCTTGGAGTGTGTCACAGATGTCCAGTG 1643  
 DB 1441 CAGAACGAAACAGATCGAAGGGCATTTCTTGGAGTGTGTCACAGATGTCCAGTG 1500  
 OY 1644 AAAAGAACTTCTGAAGACATCTCCCAATTAAGATTGAGGATTCAGGCTTATGCTT 1703  
 DB 1501 AAAAGAACTTCTGAAGACATCTCCCAATTAAGATTGAGGATTCAGGCTTATGCTT 1560  
 OY 1704 ATCACAAATATGGRATATTCCTGACGCGCATCCGGAACCTCAGGCTGCTGACGA 1763  
 DB 1561 ATCACAAATATGGRATATTCCTGACGCGCATCCGGAACCTCAGGCTGCTGACGA 1620  
 OY 1764 AAAAGCGAAGAAACCTTAATATAGTAGTACCTTCTGAGAGTGTGAGGGAAGAC 1823  
 DB 1621 AAAAGCGAAGAAACCTTAATATAGTAGTACCTTCTGAGAGTGTGAGGGAAGAC 1680  
 OY 1824 CGAGATGACGTTTGAAGAATCTATGCTGAATCGAAGACGCGGAAGTTTTCATGAG 1883  
 DB 1681 CGAGATGACGTTTGAAGAATCTATGCTGAATCGAAGACGCGGAAGTTTTCATGAG 1740  
 OY 1884 GTGAAGAAGACAGTGACAAAGGGAAGCGGTTTGGTGATGACAAATGACATATAT 1943  
 DB 1741 GTGAAGAAGACAGTGACAAAGGGAAGCGGTTTGGTGATGACAAATGACATATAT 1800  
 OY 1944 ACAGACATCAAGGCTACTCTTTCAGTTAGTGTGAGGCGTTTCCAGAGTCAATGGGAAA 2003  
 DB 1801 ACAGACATCAAGGCTACTCTTTCAGTTAGTGTGAGGCGTTTCCAGAGTCAATGGGAAA 1860  
 OY 2004 TATTTCTTCCGAGGAATGTAACTCAAGAGAGGCTGACATGACTTGAACATCCGAT 2063  
 DB 1861 TATTTCTTCCGAGGAATGTAACTCAAGAGAGGCTGACATGACTTGAACATCCGAT 1920



OY	2064	GTGTCCTTGGGAGATGANTGGTCCACTGCAACACACTGACCTTACACCTTGAGCCACCCGCAAT	2123
Db	1921	GTGTCTCTTGCGAGATGATATGGTCTCTACTGCAACACTGTGACCTACACCCGTGACACACCGCAAT	1980
OY	2124	CTGTCTCAGTTAGAAAGCGCATTAAGCTCTACCTTAAAGGCAAGAAACCTCTCTCCAGGT	2183
Db	1981	CTGTCTCAGTTAGAAAGCGCATTAAGCTCTACCTTAAAGGCAAGAAACCTCTCTCCAGGT	2040
OY	2184	GATTAAGAATTGATCTCAAGAAAGTCCCTTTTGTAGCGGGGTGTGAGTGGCCCCCATTTGAAGCG	2243
Db	2041	GATTAAGAATTGATCTCAAGAAAGTCCCTTTTGTAGCGGGGTGTGAGTGGCCCCCATTTGAAGCG	2100
OY	2244	TATTGAGCACCGTGGGCCCTCCAAACAATCTGTAAAAATTTCTGCAAGGGCGTGTGAGGTTGGC	2303
Db	2101	TATTGAGCACCGTGGGCCCTCCAAACAATCTGTAAAAATTTCTGCAAGGGCGTGTGAGGTTGGC	2160
OY	2304	TTTCCTCGGCACTCGCACGGGCGCTCTCCAGATCAACCTGTTTGTGCGGGCGTGAGCACCTC	2363
Db	2161	TTTCCTCGGCACTCGCACGGGCGCTCTCCAGATCAACCTGTTTGTGCGGGCGTGAGCACCTC	2220
OY	2364	ACCAATCAGGACTTCTCTGAAAGCTGGCGAGACAGGAGAACTTTTAAACGACAGACATTTTC	2423
Db	2221	ACCAATCAGGACTTCTCTGAAAGCTGGCGAGACAGGAGAACTTTTAAACGACAGACATTTTC	2280
OY	2424	CCCTCTGTGGTACCGAAGAGCGCGTGAGACACATTTCCAGGGAGCTTCTGTACTGTGATCCCA	2483
Db	2281	CCCTCTGTGGTACCGAAGAGCGCGTGAGACACATTTCCAGGGAGCTTCTGTACTGTGATCCCA	2340
OY	2484	TTTCAGCAGCTGGACAGTCAATTAAGAAAGATGTGTGCACACAGTACATCCATCCAGAGTC	2543
Db	2341	TTTCAGCAGCTGGACAGTCAATTAAGAAAGATGTGTGCACACAGTACATCCATCCAGAGTC	2400
OY	2544	CTGGATTAACGGGAATTTCTCTGTGTGGGACGCTGTAGGCAATTCAGATGAACTTGAATTT	2603
Db	2401	CTGGATTAACGGGAATTTCTCTGTGTGGGACGCTGTAGGCAATTCAGATGAACTTGAATTT	2460
OY	2604	TTTCCAAAGGAAGTTCTTGAGACTGCGCACAGACAGTGTGCTTCCCTGGATGGCAATGCTCC	2663
Db	2461	TTTCCAAAGGAAGTTCTTGAGACTGCGCACAGACAGTGTGCTTCCCTGGATGGCAATGCTCC	2520
OY	2664	ATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATAGACAAATTAATGATTTATTTTG	2723
Db	2521	ATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATAGACAAATTAATGATTTATTTTG	2580
OY	2724	GTGTCTGAAAGACTACACAGACTGTGAGACTTTTTTGTGAGATCGAGGAGCTGTGATG	2783
Db	2581	GTGTCTGAAAGACTACACAGACTGTGAGACTTTTTTGTGAGATCGAGGAGCTGTGATG	2640
OY	2784	AACCAATTTCTCTAAACATGGGCTCTTTTAAACAAATTAACCTTTATGACTTACCAAGCCATG	2843
Db	2641	AACCAATTTCTCTAAACATGGGCTCTTTTAAACAAATTAACCTTTATGACTTACCAAGCCATG	2700
OY	2844	TGTAGACCCACACAGGAAGACAGCATGGCGGCCCATGAGGCTCTGTGATCTCTATTAATGCC	2903
Db	2701	TGTAGACCCACACAGGAAGACAGCATGGCGGCCCATGAGGCTCTGTGATCTCTATTAATGCC	2760
OY	2904	TTTCCTCTCGCAGTAAATATGATTCATGACAGAACTTGTCTTGTCTGTGGAAATTTAAC	2963
Db	2761	TTTCCTCTCGCAGTAAATATGATTCATGACAGAACTTGTCTTGTCTGTGGAAATTTAAC	2820
OY	2964	CTTCTCAGTTGGTGGCACCTCCGATATGACAGCTTAAAGCCGCAAAATTTCAACACACCTCG	3023
Db	2821	CTTCTCAGTTGGTGGCACCTCCGATATGACAGCTTAAAGCCGCAAAATTTCAACACACCTCG	2880
OY	3024	GAGCCTTGTGATCTGAATATTCACAGACTTCTCTGTAGGCGACACATCAAGGAGACTACA	3083
Db	2881	GAGCCTTGTGATCTGAATATTCACAGACTTCTCTGTAGGCGACACATCAAGGAGACTACA	2940
OY	3084	GGGAATATTGCTTGTGGAAGACTGCTCCAAAGTCTTTTGTATCATCAGCAAAATCCCAAGCAGC	3143
Db	2941	GGGAATATTGCTTGTGGAAGACTGCTCCAAAGTCTTTTGTATCATCAGCAAAATCCCAAGCAGC	3000
OY	3144	AACCTGTTTCATGTGTGTGTGGACACAGCAGTGCCTCTGTGAATTTGTGGCCCCCATTCACC	3203

[illegible]



Db 541 AAAGACCTGCAATGTAATGGGTTATGGTCTGAATCTTAACAAACATTTTGTGA 600  
Qy 744 GATACTTTGACCCGTGACCATCTCTCATATGCGAGTACTTTGGAAGTCAAAAGGCTT 803  
Db 601 GATACTTTGACCCGTGACCATCTCTCATATGCGAGTACTTTGGAAGTCAAAAGGCTT 660  
Qy 804 TTTAGGCAATCCGGGATTTAAATGGAGCCAGATGAAATGAGTCAATGCTTCGAC 863  
Db 661 TTTAGGCAATCCGGGATTTAAATGGAGCCAGATGAAATGAGTCAATGCTTCGAC 720  
Qy 864 TGCAGAACCCGAAATGGTATCATCCAGCAGCACTTCCGAAAGAGTGTCTTTTA 923  
Db 721 TGCAGAACCCGAAATGGTATCATCCAGCAGCACTTCCGAAAGAGTGTCTTTTA 780  
Qy 924 GTTACGCTGATGCGAGATGAAAGACCTCCGTGACTATCCGAGCAACACTCTCA 983  
Db 781 GTTACGCTGATGCGAGATGAAAGACCTCCGTGACTATCCGAGCAACACTCTCA 840  
Qy 984 TCCATTTTGGATACACTTTGGGATGATGACTTCTTCAACATTAATGCTTATAGAGAG 1043  
Db 841 TCCATTTTGGATACACTTTGGGATGATGACTTCTTCAACATTAATGCTTATAGAGAG 900  
Qy 1044 CTTCACATTTGGAACCTTGCTGCTGAATGGAACCTTTGTCGAAGCCGACAGCAAA 1103  
Db 901 CTTCACATTTGGAACCTTGCTGCTGAATGGAACCTTTGTCGAAGCCGACAGCAAA 960  
Qy 1104 GAGCACTTCAGGAGACATCTGAGCAAACTTTTCCGCAAAAGATTTGGAATGATTA 1163  
Db 961 GAGCACTTCAGGAGACATCTGAGCAAACTTTTCCGCAAAAGATTTGGAATGATTA 1020  
Qy 1164 GCTGTGAATGAGGCTTCAACATTTCTGAGTATTTCAACCAACAGGAGCAAGAGATC 1223  
Db 1021 GCTGTGAATGAGGCTTCAACATTTCTGAGTATTTCAACCAACAGGAGCAAGAGATC 1080  
Qy 1224 TGCAGTCAAGCCATCATGCTATTAATGATGAGGCGGTGAGCAACCTTATGATCAATCTTT 1283  
Db 1081 TGCAGTCAAGCCATCATGCTATTAATGATGAGGCGGTGAGCAACCTTATGATCAATCTTT 1140  
Qy 1284 GCAAAATACAAATTTGGCCAGATCGAAAGGTTGCGATCTTCAATACCTATGAGAGAGAG 1343  
Db 1141 GCAAAATACAAATTTGGCCAGATCGAAAGGTTGCGATCTTCAATACCTATGAGAGAGAG 1200  
Qy 1344 GCTGCTTTGAGACAAATCTAAAGTGATGCGCTGTGCGCAAAAGATTTTATACCAG 1403  
Db 1201 GCTGCTTTGAGACAAATCTAAAGTGATGCGCTGTGCGCAAAAGATTTTATACCAG 1260  
Qy 1404 ATCTCCACCTTGGCTGATGTGACAGAGAAATGTCAATGCAATACCTTACGCTTACGCGG 1463  
Db 1261 ATCTCCACCTTGGCTGATGTGACAGAGAAATGTCAATGCAATACCTTACGCTTACGCGG 1320  
Qy 1464 CCCAAATGATCGACAGAGACATGATGTGTTGAGCCGAAAGCTTCAATGAGACAGACT 1523  
Db 1321 CCCAAATGATCGACAGAGACATGATGTGTTGAGCCGAAAGCTTCAATGAGACAGACT 1380  
Qy 1524 CTGACTGATGATCGAGGCGCCGCTCTGATGACCACTGATGACCATGCTGTATTAAG 1583  
Db 1381 CTGACTGATGATCGAGGCGCCGCTCTGATGACCACTGATGACCATGCTGTATTAAG 1440  
Qy 1584 CAGACGAAACAGATGGAAGGCGATTTCTTGGAGTGGTGGACAGATGTCACAGTG 1643  
Db 1441 CAGACGAAACAGATGGAAGGCGATTTCTTGGAGTGGTGGACAGATGTCACAGTG 1500  
Qy 1644 AAAGACCTTGAAGACATCCCAATACAAATTTAGGAGTTCAGGTTATGCTTTGCA 1703  
Db 1501 AAAGACCTTGAAGACATCCCAATACAAATTTAGGAGTTCAGGTTATGCTTTGCA 1560  
Qy 1704 ATCACAATATATGRTATATCTGACGACATCCGAGACTGAGGCTGTATAGAAAGGA 1763  
Db 1561 ATCACAATATATGRTATATCTGACGACATCCGAGACTGAGGCTGTATAGAAAGGA 1620  
Qy 1764 AAAAAGGAAGAACTAATATAGTGAAGCTTCTCTGAGTGGAATGGGAAGAC 1823  
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Db 1621 AAAAGCGAAGAAACCTAATATAGTAGCTTGACCTCTGAGTGGATGGGAAGAC 1680  
Qy 1824 CGAGATGACGTGTGAGAAATCTATGGGATTCGAAGAGCGGGAAAGTTTCCATGGAG 1883  
Db 1681 CGAGATGACGTGTGAGAAATCTATGGGATTCGAAGAGCGGGAAAGTTTCCATGGAG 1740  
Qy 1884 GTGAAGAGACAGTGGACAAAGGGAAGGGGTTTGGTATGATCAAAATGACTACTATAT 1943  
Db 1741 GTGAAGAGACAGTGGACAAAGGGAAGGGGTTTGGTATGATCAAAATGACTACTATAT 1800  
Qy 1944 ACAGACATCAAGGATCTCTTCACTTATAGTGTGGCGCTTCCAGAGTCAATGGGAA 2003  
Db 1801 ACAGACATCAAGGATCTCTTCACTTATAGTGTGGCGCTTCCAGAGTCAATGGGAA 1860  
Qy 2004 TATTTCTCCGGGGAATGATACCATCGAAGAGGCTCGATGACTTGAACATCCCAT 2063  
Db 1861 TATTTCTCCGGGGAATGATACCATCGAAGAGGCTCGATGACTTGAACATCCCAT 1920  
Qy 2064 GTGTCTTGGCAGATGAATGGTCTACTGCAACACTGACCTACACCTGAGCAGCCCAT 2123  
Db 1921 GTGTCTTGGCAGATGAATGGTCTACTGCAACACTGACCTACACCTGAGCAGCCCAT 1980  
Qy 2124 CTGTCTCAGTTAGAAAGCAATTAAGCTTAACCTTAAAGCAAGAAACCTGTCTCAAGT 2183  
Db 1981 CTGTCTCAGTTAGAAAGCAATTAAGCTTAACCTTAAAGCAAGAAACCTGTCTCAAGT 2040  
Qy 2184 GATAAAGAAATTCATCCAGAAATGCTTTTGAACGGGCTGTGAGTCCCATTTAAGC 2243  
Db 2041 GATAAAGAAATTCATCCAGAAATGCTTTTGAACGGGCTGTGAGTCCCATTTAAGC 2100  
Qy 2244 TATTGGACACGCTGGCCCTCAACAAATCTGAAATTTCTGCAAGAGGCTGAGAGTTC 2303  
Db 2101 TATTGGACACGCTGGCCCTCAACAAATCTGAAATTTCTGCAAGAGGCTGAGAGTTC 2160  
Qy 2304 TTCTCTGACACTCGACAGGCGCTCTCAGAAATCAACCTGTTTGTGCGGCTGAGAGCTC 2363  
Db 2161 TTCTCTGACACTCGACAGGCGCTCTCAGAAATCAACCTGTTTGTGCGGCTGAGAGCTC 2220  
Qy 2364 ACCATCAGAGACTTCTTAAAGCTGTGGCCAGCAAGGAAACATTTTAAACGACAGACATTC 2423  
Db 2221 ACCATCAGAGACTTCTTAAAGCTGTGGCCAGCAAGGAAACATTTTAAACGACAGACATTC 2280  
Qy 2424 CCTCTCTGTACCGAAGAGCGCTGAGAGATTCAGAGGAGCTTCTACTCGATCCCA 2483  
Db 2281 CCTCTCTGTACCGAAGAGCGCTGAGAGATTCAGAGGAGCTTCTACTCGATCCCA 2340  
Qy 2484 TTCAGACCTGAGACAGTCAATTAAGCAATGTGTGACAGCAAGTACATCCATCAGCTC 2543  
Db 2341 TTCAGACCTGAGACAGTCAATTAAGCAATGTGTGACAGCAAGTACATCCATCAGCTC 2400  
Qy 2544 CTGATGAAAGGAAATCTCTGTGTGTGACACTGTAGCATTCAGATGAACCTGAATTT 2603  
Db 2401 CTGATGAAAGGAAATCTCTGTGTGTGACACTGTAGCATTCAGATGAACCTGAATTT 2460  
Qy 2604 TTCCAAAGAGAGTTCTGAGACCTGCCAGCAGACAGTGTGCTTCCGGAATGGGAATGCTCC 2663  
Db 2461 TTCCAAAGAGAGTTCTGAGACCTGCCAGCAGACAGTGTGCTTCCGGAATGGGAATGCTCC 2520  
Qy 2664 ATCAGCTGTGATGATGAGACTGTGAATTTTAACTCATAGCAATTAATGATTAATTTG 2723  
Db 2521 ATCAGCTGTGATGATGAGACTGTGAATTTTAACTCATAGCAATTAATGATTAATTTG 2580  
Qy 2724 GTGTCTGAAGCTACACACAGACTGAGACTTTTGTGTGATGAGAGAGCTGTATG 2783  
Db 2581 GTGTCTGAAGCTACACACAGACTGAGACTTTTGTGTGATGAGAGAGCTGTATG 2640  
Qy 2784 AACAAATTTGCTAACAATGAGGCTCTTTAAAGAAATTAACCTTATGATACCAAGCATG 2843  
Db 2641 AACAAATTTGCTAACAATGAGGCTCTTTAAAGAAATTAACCTTATGATACCAAGCATG 2700  
Qy 2844 TGTAGAGCCAAACAAGAGAGGATGGGCGCCATGCTCTGATCTTATTAATGCC 2903  
Db 2701 TGTAGAGCCAAACAAGAGAGGATGGGCGCCATGCTCTGATCTTATTAATGCC 2760  
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Db	241	GAATTTGATGAGCCTCCAACTGGTAAAGAAAGCTGGCAAGAACATATGAAAGATGTTTCAC	300
QY	444	AAGAACTGAGAGCCCTCAGCGCTGTGGTGAAGCTGCAGAAGACACACTGAAACAT	503
Db	301	AAAGAACTGAGAGCCCTCAGCGCTGTGGTGAAGCTGCAGAAGACACACTGAAACAT	360
QY	504	GAATTTGATGAGACTTATGATGATGAATATCTTCAATGCTGTGCGATTAATGAAAGGAC	563
Db	361	GAATTTGATGAGACTTATGATGATGAATATCTTCAATGCTGTGCGATTAATGAAAGGAC	420
QY	564	AAAGACGGAAATTTTTTGGAGCTGGGAAAAGAAATTCATCTTAGCCCAATGACATTTT	623
Db	421	AAAGACGGAAATTTTTTGGAGCTGGGAAAAGAAATTCATCTTAGCCCAATGACATTTT	480
QY	624	AATAATTTGCGTGAACATCGCTAAGTAGACGTCCAAAGTACCACGAACATGTACAC	683
Db	481	AATAATTTGCGTGAACATCGCTAAGTAGACGTCCAAAGTACCACGAACATGTACAC	540
QY	684	AAAGACCCCTGCATTTGTCAATGGGGTTATTGTGCTGAATCTCAATCAAGTTTTTGT	743
Db	541	AAAGACCCCTGCATTTGTCAATGGGGTTATTGTGCTGAATCTCAATCAAGTTTTTGT	600
QY	744	GATTACTTTGACCCGTGACCCATCTCTCATATGCAATCTTTGGAAAGTCAAAAGGCTTT	803
Db	601	GATTACTTTGACCCGTGACCCATCTCTCATATGCAATCTTTGGAAAGTCAAAAGGCTTT	660
QY	804	TTTAAAGCAGTATCCGGGGATTAAATGGGAACCATATGAATGAGATCTTGCCTTCGAC	863
Db	661	TTTAAAGCAGTATCCGGGGATTAAATGGGAACCATATGAATGAGATCTTGCCTTCGAC	720
QY	864	TTCCAGAACCCGAAATGATCATCCAGCAGCAACTTCTCCGAAAGACGTGTCAATTTTA	923
Db	721	TTCCAGAACCCGAAATGATCATCCAGCAGCAACTTCTCCGAAAGACGTGTCAATTTTA	780
QY	924	GTTGACGTCAGAGGCGATGAAGAGACTCGCTGTGACTTCCCGAAGCAACACGTCTTA	983
Db	781	GTTGACGTCAGAGGCGATGAAGAGACTCGCTGTGACTTCCCGAAGCAACACGTCTTA	840
QY	984	TCCATTTTGGATATACACTTTGGGATGATGAGACTCTTTCACATTAATTTGCTATATAGAGAG	1044
Db	841	TCCATTTTGGATATACACTTTGGGATGATGAGACTCTTTCACATTAATTTGCTATATAGAGAG	900
QY	1044	CTTCACTATGTGGAACCTTGCTGTGAATGGAACCTTGTGTGCAACCGCAGCAGCAAAACA	1103
Db	901	CTTCACTATGTGGAACCTTGCTGTGAATGGAACCTTGTGTGCAACCGCAGCAGCAAAACA	960
QY	1104	GAGCACTTCAGGAGCAATCTGAGCAAAACCTTTGGCAAAAGAAATGGAATGTTGATATA	1166
Db	961	GAGCACTTCAGGAGCAATCTGAGCAAAACCTTTGGCAAAAGAAATGGAATGTTGATATA	1020
QY	1164	GCTCTGAATGAGGCTTCAACATTTCTGAGTATTTCAACACACGCGGACAAAGAGTATC	1223
Db	1021	GCTCTGAATGAGGCTTCAACATTTCTGAGTATTTCAACACACGCGGACAAAGAGTATC	1080
QY	1224	TGCGAGTAGGCGCATATGCTCATTAATGATGGGGCGGTGAGCAACTATGATATCAATCTTT	1283
Db	1081	TGCGAGTAGGCGCATATGCTCATTAATGATGGGGCGGTGAGCAACTATGATATCAATCTTT	1140
QY	1284	GCAAAATATCAATTTGGCCAGATTCGAAAGGTTTGCATTTACATTAATCTTATGAGCAGAG	1343
Db	1141	GCAAAATATCAATTTGGCCAGATTCGAAAGGTTTGCATTTACATTAATCTTATGAGCAGAG	1200
QY	1344	GCTGCGTTTGCAGACATCTAAAGTGTGATGGCTGTGCCAACAAAGATTTTTTACCAG	1403
Db	1201	GCTGCGTTTGCAGACATCTAAAGTGTGATGGCTGTGCCAACAAAGATTTTTTACCAG	1260
QY	1404	ATCTCCACCTTTGGCTATGTGCGAGGAGATGTGCATGGAATGCTTACAGTCTTAAGCGG	1463
Db	1261	ATCTCCACCTTTGGCTATGTGCGAGGAGATGTGCATGGAATGCTTACAGTCTTAAGCGG	1320
QY	1464	CCCAAAATCATGACAGGAGCATGATGTGTGTGGACCGAAGCTTACATTTAGCAGCACT	1523
Db	1321	CCCAAAATCATGACAGGAGCATGATGTGTGTGGACCGAAGCTTACATTTAGCAGCACT	1380

QY 1524 CTGACTGATGATCAGGGCCCGCTCTGATGACCACTGTAGCCATGCTGTCTGTAGTAAG 1583  
 DB 1381 CTGACTGATGATCAGGGCCCGCTCTGATGACCACTGTAGCCATGCTGTCTGTAGTAAG 1440  
 QY 1584 CAGACGAAACCAAGTTCAGAGGGGCTCTCTGAGAGGCTGTGGACAGATGCCAGTG 1643  
 DB 1441 CAGACGAAACCAAGTTCAGAGGGGCTCTCTGAGAGGCTGTGGACAGATGCCAGTG 1500  
 QY 1644 AAGAACTTCGTAAGACCATCCCAATATACAGATTAGGGATTACGGTTTTCCTTTGA 1703  
 DB 1501 AAGAACTTCGTAAGACCATCCCAATATACAGATTAGGGATTACGGTTTTCCTTTGA 1560  
 QY 1704 ATCACAATTAATGRTATATCTCGACGATCCGGAATCAGGCTCTGTACGAGAAGA 1763  
 DB 1561 ATCACAATTAATGRTATATCTCGACGATCCGGAATCAGGCTCTGTACGAGAAGA 1620  
 QY 1764 AAAAAAGCAAGAAACCTATATATATAGCTGTGACCTCTCTGAGAGTGAAGTGGGAAGC 1823  
 DB 1621 AAAAAAGCAAGAAACCTATATATATAGCTGTGACCTCTCTGAGAGTGAAGTGGGAAGC 1680  
 QY 1824 CGAGATGACGCTGTGAGAAATGCTATGTTGTAATGGAAGAGGGGAATTTTCCATGAG 1883  
 DB 1681 CGAGATGACGCTGTGAGAAATGCTATGTTGTAATGGAAGAGGGGAATTTTCCATGAG 1740  
 QY 1884 GTGAAGAGACAGTGGACAAAGGAAAGGGTTTGTGATGACAAATATGACTATTTAT 1943  
 DB 1741 GTGAAGAGACAGTGGACAAAGGAAAGGGTTTGTGATGACAAATATGACTATTTAT 1800  
 QY 1944 ACAGACATCAAGGGTACTCTCTTCACTTGTAGTGTGGCTTTCAGAGCTCATGGGAA 2003  
 DB 1801 ACAGACATCAAGGGTACTCTCTTCACTTGTAGTGTGGCTTTCAGAGCTCATGGGAA 1860  
 QY 2004 TATTTCTTCCAGAGGAATGTAAACCATGCAAGAGGCTGCACTGACTTGAGACATCCGAT 2063  
 DB 1861 TATTTCTTCCAGAGGAATGTAAACCATGCAAGAGGCTGCACTGACTTGAGACATCCGAT 1920  
 QY 2064 GTGTCTTGGCAGATGATGCTCTTCTACTGCAACACTGACCTACACCCGAGACGCCAT 2123  
 DB 1921 GTGTCTTGGCAGATGATGCTCTTCTACTGCAACACTGACCTACACCCGAGACGCCAT 1980  
 QY 2124 CTGCTCAGTTAGAGGAGTAACTTACCTTAAAGGCAAGAACTCTGCTCCAGTGT 2183  
 DB 1981 CTGCTCAGTTAGAGGAGTAACTTACCTTAAAGGCAAGAACTCTGCTCCAGTGT 2040  
 QY 2184 GATTAAGAAATTTGATCCAAAGAGTCTTTTGTGAGCGGCTGTGAGTGTGCCCATTTGAAGCG 2243  
 DB 2041 GATTAAGAAATTTGATCCAAAGAGTCTTTTGTGAGCGGCTGTGAGTGTGCCCATTTGAAGCG 2100  
 QY 2244 TATTTGACCAAGCTGCGCTCAACAAATCTGAAATTTCTGCAAGGCGGTGAGGTTGCC 2303  
 DB 2101 TATTTGACCAAGCTGCGCTCAACAAATCTGAAATTTCTGCAAGGCGGTGAGGTTGCC 2160  
 QY 2304 TTTCTCTGGCAGCTGCGACGGGCTCTCTCCAGATCAACCTGTTTGTGGGGC TGAGCAGCTC 2363  
 DB 2161 TTTCTCTGGCAGCTGCGACGGGCTCTCTCCAGATCAACCTGTTTGTGGGGC TGAGCAGCTC 2220  
 QY 2364 ACCAATCAGAGCTTCTCTGAAAGCTGGGGAAGAAGAACTTTTAAACGCGAGCAGATTTC 2423  
 DB 2221 ACCAATCAGAGCTTCTCTGAAAGCTGGGGAAGAAGAACTTTTAAACGCGAGCAGATTTC 2280  
 QY 2424 CTTCTCTGTTACGGAAGAGCGCTGAGCAGATTCAGAGGAGCTTCTGCTATCTGATCCCA 2483  
 DB 2281 CTTCTCTGTTACGGAAGAGCGCTGAGCAGATTCAGAGGAGCTTCTGCTATCTGATCCCA 2340  
 QY 2484 TTTGAGACTGAGACAGTCAATTAAGCAATGTGTGACAGCAAGTATCATCCAGCTC 2543  
 DB 2341 TTTGAGACTGAGACAGTCAATTAAGCAATGTGTGACAGCAAGTATCATCCAGCTC 2400  
 QY 2544 CTGAGTGAAGCAAGAAATCTCTGTTGTTGGCAGCTGTAGGCAATTGAGTGAATTT 2603  
 DB 2401 CTGAGTGAAGCAAGAAATCTCTGTTGTTGGCAGCTGTAGGCAATTGAGTGAATTT 2460

QY 2604 TTCAAAGGAAGTTCGAGCTGCGACAGACAGATGCTTCCCTGGATGGCAATGCTCC 2663  
 DB 2461 TTCAAAGGAAGTTCGAGCTGCGACAGACAGATGCTTCCCTGGATGGCAATGCTCC 2520  
 QY 2664 ATTCAGCTGATGATGAGACTGTGAATTTGTACTCATATAGCAATTAATGATTTATTTG 2723  
 DB 2521 ATTCAGCTGATGATGAGACTGTGAATTTGTACTCATATAGCAATTAATGATTTATTTG 2580  
 QY 2724 GTGTCTGAAGACTATACACAGACTGGAGACTTTTGTGTGATGAGAGGAGCTGTGATG 2783  
 DB 2581 GTGTCTGAAGACTATACACAGACTGGAGACTTTTGTGTGATGAGAGGAGCTGTGATG 2640  
 QY 2784 AACCAATTTGCTAACATGGGCTCTTAAAGAAATTAACCTTTATGACTACCAACCATG 2843  
 DB 2641 AACCAATTTGCTAACATGGGCTCTTAAAGAAATTAACCTTTATGACTACCAACCATG 2700  
 QY 2844 TGTAGAGCCAAACAGAAAGCAGCATGGCGCCCATATGGCTCTGATATCATATATG 2903  
 DB 2701 TGTAGAGCCAAACAGAAAGCAGCATGGCGCCCATATGGCTCTGATATCATATATG 2760  
 QY 2904 TTTCTCTCTGACGTAATAATGATATGACAGAACTGTCTGTTGCTGTGGAATTTAAC 2963  
 DB 2761 TTTCTCTCTGACGTAATAATGATATGACAGAACTGTCTGTTGCTGTGGAATTTAAC 2820  
 QY 2964 CTCTGAGTTGTGTGCTGCTCCATATGACAGTAAAGCCCAAAATTTGAACAGCCTG 3023  
 DB 2821 CTCTGAGTTGTGTGCTGCTCCATATGACAGTAAAGCCCAAAATTTGAACAGCCTG 2880  
 QY 3024 GAGCCTTGTATACGATATATACAGATTCCTCTGTGAGCGGACCATCAAGAGACTACA 3083  
 DB 2881 GAGCCTTGTATACGATATATACAGATTCCTCTGTGAGCGGACCATCAAGAGACTACA 2940  
 QY 3084 GGGATATATTTCTTGTGAAGACTGCTCAAGTCTTGTGTATCATCAGCAATCCCAAGCAGC 3143  
 DB 2941 GGGATATATTTCTTGTGAAGACTGCTCAAGTCTTGTGTATCATCAGCAATCCCAAGCAGC 3000  
 QY 3144 AACCTGTATGATGTTGTGTGTGAGAGCAGCTGCTCTGTGATCTGTGTGCCCCATC 3200  
 DB 3001 AACCTGTATGATGTTGTGTGTGAGAGCAGCTGCTCTGTGATCTGTGTGCCCCATC 3057  
  
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 AX099302  
 LOCUS AX099302 3057 bp DNA linear PAT 02-Apr-2001  
 DEFINITION Sequence 7 from Patent WO0120336.  
 ACCESSION AX099302  
 VERSION AX099302.1 GI:13538464  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3057)  
 AUTHORS Bertelli,F., Brown,J.P., Dissanayake,V., Suman-Chauhan,N. and  
 Gee,N.S.  
 TITLE Screening for alpha2delta-1 subunit binding ligands  
 JOURNAL Patent: WO 0120336-A 7 22-MAR-2001;  
 WARNER-LAMBERT COMPANY (US)  
 FEATURES  
 source location/Qualifiers  
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 BASE COUNT 848 a 692 c 778 g 738 t 1 others  
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 Query Match 81.1%; Score 3056.6; DB 6; Length 3057;  
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 Matches 3057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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OY	264	GTGCTGAAGCTCTGGGCTCTCGGCTTTTGGTGGGGAGATAAATCCATTGGCTCAATAC	323
Db	121	GTGCTGAAGCTCTGGGCTCTCGGCTTTTGGTGGGGAGATAAATCCATTGGCTCAATAC	180
OY	324	TCCGGTTCCAGCTTCTGGCAAAAGAAATCAAGAGATGAGAAAGACGTTGCCATGAA	383
Db	181	TCCGGTTCCAGCTTCTGGCAAAAGAAATCAAGAGATGAGAAAGACGTTGCCATGAA	240
OY	384	GAATTTGATGGGCTCCCAACTGGTAAAGAAAGCTGGCAAAAGACATGGAAGAGATGTTTCAC	443
Db	241	GAATTTGATGGGCTCCCAACTGGTAAAGAAAGCTGGCAAAAGACATGGAAGAGATGTTTCAC	300
OY	444	AMGAGCTGAGGCGCGTCAGGCGCTGGTGGAGGCTGAGAAAGACACCTGAAACAT	503
Db	301	AMGAGCTGAGGCGCGTCAGGCGCTGGTGGAGGCTGAGAAAGACACCTGAAACAT	360
OY	504	GAATTTGATGCACTTACAGTATGCAATACCTTCAATGCTGTGCTGATAAATGAAAGGAC	563
Db	361	GAATTTGATGCACTTACAGTATGCAATACCTTCAATGCTGTGCTGATAAATGAAAGGAC	420
OY	564	AAAGACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATTAGCCCCAATGACATTTT	623
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OY	624	AATTAATTTGGCTGTGACATCAGTCTAAGTACGCTCCAACTACCAAGCAATGTAACAC	683
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OY	684	AAAGACCGTCGCAATTTGTCAATGGGGTTTATTGGTGAATCTGTAAACAAAGTTTTGTA	743
Db	541	AAAGACCGTCGCAATTTGTCAATGGGGTTTATTGGTGAATCTGTAAACAAAGTTTTGTA	600
OY	744	GATTAATCTTGAACCGTGACCCATCTCATATGGCAGTACTTTGGAGTGCMAAGGCTTT	803
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OY	804	TTTACGACGATATCCGGGGATTAAATGGGAACACAGATAGAGATGAGTCAATGGCTTCGAC	863
Db	661	TTTACGACGATATCCGGGGATTAAATGGGAACACAGATAGAGATGAGTCAATGGCTTCGAC	720
OY	864	TGCAGGAAACCCAAAATGATGATCTCAGGACAGCAATTTCTCCGAAGACGTGCTCATTTTAA	923
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OY	984	TCCATTTTGGATACACTTGGGGATGATGACTTTTCAACATAATATGCTTAATAGAGAG	1043
Db	841	TCCATTTTGGATACACTTGGGGATGATGACTTTTCAACATAATATGCTTAATAGAGAG	900
OY	1044	CTTGACATGTGGAACCTTTCGCTGAATGGAACCTTTGGTCCAAGCCGACAGCAAAACAA	1103
Db	901	CTTGACATGTGGAACCTTTCGCTGAATGGAACCTTTGGTCCAAGCCGACAGCAAAACAA	960
OY	1104	GAGCAGCTTACAGGAGCAATCTGGACAAACCTTTTCCCAAAAGAAATTTGGAATGTATA	1163
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OY	1164	GCTCTGAATGAGGCTTCAACATTTCTGAGTGAATTTCAACACACGCGGACAAAGAAATTC	1223
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OY	1224	TGCAGTCAGGCCATCATGCTCATTAACATGATGGGGGCTGGACACCTATGATATCAATCTTT	1283
Db	1081	TGCAGTCAGGCCATCATGCTCATTAACATGATGGGGGCTGGACACCTATGATATCAATCTTT	1140
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Db	1141	GCMAAATTCATTTGGCCGAGATCGAAAGTTCCGCTTTCCACATTAATCTTATGGACGAG	1200
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Db	1201	GCTGCGTTTGCAGACAATCTAAAGTGGATGGCCGTGTCCTCCAAAGAGATTTTTTACCAG	1260
Qy	1404	ATCTCCACCTTGGCGTGAATGTGCAGAGAAATGTCAATGAAATACCTTCACTGCTTTAGCCG	1463
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Qy	1524	CTGACTGATGATCAGGGGCCCGCTCTGATGACCACTGTAGCCATGCTGTATTAGTAAG	1583
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Db	1441	CAGAACCAAAACGAGATCGAAGGGCATTTCTTCTGGAGATGTTGTGCAACAGATGTCACATG	1500
Qy	1644	AAAGAACTTCTGAAAGACCATCCCAATAACATTTAGGGATTCAGGGTATGCGTTTGA	1703
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Qy	1704	ATCAAAATATGATGGATTAATCTGACGACATCCGAACTCAGGCTGCTGTACGAAGA	1763
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Qy	1944	ACGACATCAAGGCTACTCTCTTCAAGTTTAAAGTGTGCGCTTCCAGAGGTCATGGAAA	2003
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ACCESSION AJ010949  
VERSION AJ010949.1 GI:4186072  
KEYWORDS calcium channel alpha-2-delta-C subunit.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3710)  
AUTHORS Klugbauer, N.  
TITLE Direct Submission  
JOURNAL Submitted (10-SEP-1998) Klugbauer N., Institut fuer Pharmakologie und Toxikologie, Technische Universitaet Muenchen, Biedersteiner Str. 29, 80802, GERMANY

REFERENCE 2 (bases 1 to 3710)  
AUTHORS Klugbauer, N., Lacinova, L., Marais, E., Hobom, M., and Hofmann, F.  
TITLE Molecular diversity of the calcium channel alpha2delta subunit  
JOURNAL J. Neurosci. 19, 648-691 (1999)  
FEATURES  
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Best Local Similarity 88.5%; Pred. No. 0;  
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OY	2419	ATTTCCTCTGTGTACCGAAGAGCGGTGACAGATTCTCAGAGGACTTCCGTCTACTGGA	2478
Db	2391	ATTTCCTCTGTGTGTACGAAGAAGGTGGCCGACACATGTGCAAGAGACTTTGTCTATTCCA	2450
OY	2479	TCCCATTTACGACTGGACCGATCAATTAAGCAATGTGGTGACAGACAGTAGTACATCCATCC	2538
Db	2451	TCCCATTTTACGACAGACAGACATCAACAAAGCAATGTGGTGACAGACAGTAGTACATCC	2510
OY	2539	ACCTCTGGATGAAGGAATATCTCTGTGTGTGGCAGCTGTAGGCATTTCAGATGAACCTTG	2598
Db	2511	ACCTCTGGATGAAGGAATATCTCTCTGTGTGTGGCAGCTGTAGGCATTTCAGATGAACCTTG	2570
OY	2599	AATTTTCCAAAGGAAGTTCTGAGACTGCGACAGACAGATGTGCTTCCCTGTGATGGCAAT	2658
Db	2571	AATTTTCCAAAGGAAGTTCTGAGACTGCGACAGACAGATGTGCTTCCCTGTGATGGCAAT	2630
OY	2659	GCTCCATCAGCTGTGTATGATGAGACTGTGAATTTGTTACTCTATAGACAATTAATGGATTTA	2718



Db	2631	GCCTCATTAAAGCTGGATGATGAGAGACCTGTGAACCTTTACCTTATATGACATTAACGATTCA	2630
QY	2719	TTTTGGTGTCTGAAAGCTACACACAGCTGGAGACTTTTTTGGTGAATCGAGGAGCTG	2778
Db	2691	TTCTGGGTCTGTAAGACTACACACAGACTGGAGATTTTTTTGGTAGGTGAAGAGACTG	2750
QY	2779	TGATGAACAAATTGCTTAACATGGGCTCTTTAAAGAAATTACCTTTATATCTAACAG	2838
Db	2751	TCATGAACAAAGTTGTATACAAATGGGTTCTTTAAAGAAATTAACCTTTATACATCCAG	2810
QY	2839	CCATGTCTAGAGCCACACAGAAAGACAGCATGGCGCCATGGCTCTGTGATCTCTATA	2898
Db	2811	CCATGTGTATAGCCACACAGAGAGACGTGACGTACGTGCCCCATGGACTTGTGAGCCCTATA	2870
QY	2899	ATGCTTCTCTCTGTGCAGTAAAAATGGATTCATGACAGAACTGTCTTTGCTGGTGAAT	2958
Db	2871	AGGCTTCTCTCTCTGCGACGCAAGTGATATGACGGAACCTGTCTTCTCTGGTGGAGT	2930
QY	2959	TTTAACCTCTGCATTTGGTGGCACTCCGATATGACAGCTAAAGCCAGAAATTTGAACAGA	3018
Db	2931	TTTAACCTGTGCATTTGGTGGCACTCCGACATGACAGCTTAAGCCACAGAACTGAAACAGA	2990
QY	3019	CCCTGAGACCTTGTGATACGAAATATACACATTCGCTCTGAGCGGACATCAAGSAGA	3078
Db	2991	CCCTGAGACCTTGTGATACTGAATACCACACTTTGTTCTGAAAGCAACCATCAAGSAGA	3050
QY	3079	CTACAGGGAATATTGGCTTGTGGAAGACTGCTCCAAAGTCTTTGTATCATCAGCAAAATCCCA	3138
Db	3051	CCACAGGGAACATTCGCTTGGGAAGACTGCTCCAAAGTCTCTGTATCCAACAAATCCCGA	3110
QY	3139	GCAGCAACTGTTCAATGCTGTGTGTGTGGACAGACAGCTGCTGTGTGAATCTGTGGCCCCA	3198
Db	3111	GTACGATCTGTTCATGCTGTGTGTGTGTGGACAGTGTGTCTGTGTGAATCTGTGGCTCTTA	3170
QY	3199	TCACCATGGACACCATTTGAAATATAGATATTAATTCCTTAAGTGTGAACGCTTAAGG	3258
Db	3171	TAACCATGGACACCATTTGAAATATAGATATTAATTCCTTAAGTGTGAACGCTTTAAGG	3230
QY	3259	CCCAGAAATTCAGAAAGAGCCGCCAGAAATCTTGTATGAGCTTCCATCCCTGAGAGAGATCCAA	3318
Db	3231	CTACAGAAATTCAGAGACAGCACTCCAGAAATCTCTGACACGCTTCCATCTGAGAGAGATCCAA	3290
QY	3319	GGGAGTGTGGGGGTGCGCCGAGTCTCCAAAGCCAGACAGTCTCTCTCTGCTGCTGCTGCTG	3378
Db	3291	GAGAGTGTGGGGGTGCTGATCGAGCTTCAAGGCCAGCGGCTTGTGTCTGCTGCCCTG	3350
QY	3379	TTTTTGTGCTCTTCTCAAGCTGACACTGAGATGTTCTCTTACTGAATGAGATGTTCT	3438
Db	3351	TTTTTGTGCTCTTCTCAAGCTGACACTTACT-----ANTGGAGATGTTCT	3393
QY	3439	TCCTTGGCATGC--TAAATATGATGATTAATCTGTGAACCAAAATATGGTGCACATATAGAGA	3496
Db	3394	TTTTTGGCATGCTATTAATATATGATATGATTAATCTGTGAACCAAAATATGGTGCACATATAGAGA	3453
QY	3497	CATGAATATAGTCCAAACATCAAGCATCTTCATCATGATTTTAAACCTGTGCTGATATTAAC	3556
Db	3454	CATTAAGCATAGCCGACGCTCAGCATC--TCATGATTTTAAACGTGTGCTGATATTAAC	3510
QY	3557	TCTTAAAGATATGTTGACCAAAAAGTTATCTATTCATCTTTTACTTGTGCGAGTCAACAA	3616
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QY	3617	TGTGATTTTGGCACATGATTAATCACCCCTTCATCAGAAATGGGACCCGACATGCTGATAGCAG	3676
Db	3564	TGTGATTTTGGCACATG--ATCACCCCTTCATCAGAAATGGGAGCTGTACGTGGGTAGCAG	3620
QY	3677	TGTCCCTCTGTGCTGAACCTATTTGAACCAATTTAAACCTGTACTTTTAAATATAAG	3736
Db	3621	TGT--CCTTCTGCTTGAACCAATTTGAACCAATTTAAACCTGTACTTTTAAATATAAG	3679
QY	3737	TATATTAATTCATTAACCAAAAAA 3767	

Db	3680	TATATTAAATCTATAAAAAAAAAAAAAA	3710
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LOCUS	AX098926	3209 bp	DNA
DEFINITION	Sequence 51 from Patent WO0119870.		linear
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VERSION	AX098926.1	GI:13538143	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 3209)		
	Brown, J.P. and Bertelli, F.		
	Secreted soluble $\alpha_2(\text{I})2\text{g(d)}-2$ , $\alpha_2(\text{I})2\text{g(d)}-3$ or $\alpha_2(\text{I})2\text{g(d)}-4$		
	calcium channel subunit polypeptides and screening assays using		
	same		
JOURNAL	Patent: WO 0119870-A 51 22-MAR-2001;		
FEATURES	WARNER-LAMBERT COMPANY (US)		
source	Location/Qualifiers		
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ORIGIN	/db_xref="taxon:9606"		
	757 a 888 c 920 g 644 t		
Query Match	32.1%; Score 1211.6; DB 6; Length 3209;		
Best Local Similarity	63.6%; Pred. No. 1.5e-244;		
Matches 1932; Conservative	0; Mismatches 1069; Indels 39; Gaps 4;		
OY	250	ACATACCCGCTCCGCTGGAGACTCTGGCCCTCGGCTTTGGTGGGGAGATAAATCCA	309
Db	163	AATATCAATTCCTGGAAACAGTATGAGTACACCTTCGGCGGGCTGTATTAACA	222
OY	310	TTCCTGCTAAGTACCTCCGCTTCCAGCTTCTGCAAAAGAAATACAAAGATAGAGAAAG	369
Db	223	CTGTGACCAAAATACACGAGCTCTCTCTGCTGACAGAAAGTACAAAGATGTGAGATCCA	282
OY	370	ACGTTGCCATAGAAATAATTTGATGGCTTCCAACTGTGTAAAGAGCTGGCAAGAATCG	429
Db	283	GTCCTAAGATTCAGAGAGGTGATGCTGCTGGAGCTGTGAGAAAGTTCACAGAGACATGG	342
OY	430	AAGAGATGTTTACACAAAGTCTGAGGGCGTCAGCGCTGCTGGTGGAGGCTCAGAGAGAG	489
Db	343	AGAAATATGCTGGGGAGAAAGTCAGGGCGGTCCAAATCTGGTGGAGCTCCGAGAGAGG	402
OY	490	CACACCTGAACATGAATTTGATGCAGACTTACAGTATGAATTAATCTCAATGCTGTGCTGA	549
Db	403	CCGACCTGAACACAGATTAATGAATCCGTGGTGTGACTATTTACAACTCGGTCTCGA	462
OY	550	TAAATGAAGGACACAACGGAATTTTGGAGCTGGGAAAGAAATTCATCTTAAGCCC	609
Db	463	TCAAGGAGAGGAGACGAGAGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCTGGAGT	522
OY	610	CAAAATGACCAATTTTAATTAATTTGCTGTGGAACATCAAGTCTAAGTACGCTCAATACCA	669
Db	523	CCAATGCTCACTTACGACACTGCGGGTGAACCTCCATAGCAGCGTGAAGTGGCCA	582
OY	670	CGAAGATGTACAAACAGCCCTCAATTTGCAATGGGGTTATTTGGTCTGAATCTCTAA	729
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OY	730	ACAAAGTTTGTATGATTAATCTTGAACCTGACCATCTCTCATATGTCAGTACTTTGGAA	789
Db	643	ATGCTGCTTCTGTGAGAACTTCCAGAGAGACCCCAAGCTTGACCTGCAATATTTTGGCA	702
OY	790	GTGCAAAAGGGCTTTTAAAGGAGATGCCGGGATTAATGGGAACGAGATGAGAAATGAG	849
Db	703	GTGCAACTGATTTTCTTGAAGATCTATCAAGGTATTAATTAATGACCTGTGATGAGAAATGAG	762
OY	850	TCAATTCCTTGCAGTGCAGAAACCGAAATAGTACATCCAGGAGCAACCTTCTCCGAAG	909



Db 763 TCATTACTTTGAGTGGCGGAACCGGGCTGTGATTCAGAGCTCTACTTCTCCAAAG 822  
OY 910 ACGTGCATATTTAGTTAGTCACTGGCAGCATGAAGAAGCTCCGTGACTATCGGA 969  
Db 823 ACATAGTATTTGGTGGACGTGAGCGGCACTATGAAGGGCTGAGATTTGCCA 882  
OY 970 AGCAAAAGTCTCATCCATTTTGGATACATTTGGGAGATGATGACTCTTCAACATATTTG 1029  
Db 883 AGCAACCATATCACCACCTCTTGGACACCTGGGGGAGAAATGACTTGGTATATCATAG 942  
OY 1030 CTATTAATAGAGACTTCACTATGTGAAACCTTGCCTGAATGAACCTTGGTGAACCG 1089  
Db 943 CGTACATAGTACTACCTCATATGATGAGCTTGTTTAAAGGATCTCTCCAGGGG 1002  
OY 1090 ACAGAGCAAAACAAAGACACTTCAAGGAGCATCTGAGCAAACTTTGGCCAAAGAAATG 1149  
Db 1003 ACCGAGCAAAATCGAGAGCTTTTCAAACTGTGTGGAGAGATTTGATGATGAAGGTGG 1062  
OY 1150 GAATGTTGATATATGCTCTGTGAATGAGGCTTCAACATTTGATGATTTCAACACAGG 1209  
Db 1063 GCGTGTGTGACACACCTCTGAGAGAGCTTCCAGATCTGAACAGCTCCAAAGGCCA 1122  
OY 1210 GACAAGGAATATCTGAGTCAAGGCACTCATGCTCATTAAGTATGAGGGGCTGAGACCT 1269  
Db 1123 AGCAAGGAAGCTCTGCAACAGGCACTCATGCTCATGAGAGGGCCCTGAGAGACT 1182  
OY 1270 ATGATACAACTTTTGCAAAATACATTTGGCCAGATCGAAAGTTTGCATCTTCATACC 1329  
Db 1183 ACGAGCGGCTGTGTGAAATATTAACGTGGGCAAGCTGTAAGGTCGAGTTTCACTTACC 1242  
OY 1330 TCATTTGAGCAGAGGCTGCTTGCAGACAAATCTAAAGTATGAGGCTGTGCCAAAG 1389  
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OY 1390 GATTTTACCAGATCTCCACCTTGGCTGATGTGAGGAATGTCTAATACCTTTC 1449  
Db 1303 GCTACTACACAGCATCTCAACGCTGGGAGACCCAGGAAGATGATGATACCTGC 1362  
OY 1450 ACGTGTGAGCGGCCCAAAAGTATGACAGCAGATGATGTGTGACCGAAGCTT 1509  
Db 1363 ACGTGTCAAGCGCCCAATGTGTATCAACACAGCATCATCTGACAGAGGCTT 1422  
OY 1510 ACATTTAGCAGACTCTT-----GACTGATGATGAGGGCCCGTCGATGACCACTGTAG 1563  
Db 1423 ACATGACAGCAAGCTCTCAGCTCCAGGCTGAGAGCTGACAGTGTCCACACAGTGG 1482  
OY 1564 CCATGCTGTGTTTAAAGCAGAAAGAAACAGATCGAAGGGCTTCTTGGAGTGG 1623  
Db 1483 CCATGCACTCTTCAAGCAAGAAAGAAAGGATCCCATGGCATTTCTCTGGTGTGG 1542  
OY 1624 TTGGGACAGATGCCAGTGAAGAACTCTGAAGACCTTCCCAAAATACAGTTAGGA 1683  
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OY 1684 TTCAAGGTTATGCTTTGCAATCAAAATATGATATATCTGAGGAGCTCCGGAACCTA 1743  
Db 1603 TGCAGGATAGCCCTTTCTTGAACACCAATGCTCTCTCTCCCAATCCGAGACTTC 1662  
OY 1744 GGCTCTGTAGCAGAGAGAAAAAGCGAA---GGAAACCTAATATAGTACGTTGAGC 1800  
Db 1663 GGCCCTCTACAGAGAGGAGGAAGAACTAAACCCAAACCTAATCAACATGTGGATC 1722  
OY 1801 TCTGTAGGTGAGTGGAGAGACCCAGATGAGCTGTGGAATCTTATGTTGAAATCGAA 1860  
Db 1723 TCTCCGAAGTGGAGTGGAGAGCGAGGTGATCTCTGAGAACACCATGATCATAGGG 1782  
OY 1861 AGACGGGAGATTTTCCATGAGGTGAGAGAGAGAGTGAACAAAGGAGGAGGTTTGG 1920  
Db 1783 AAAGAGTACTCTCTCATGTGATGTGAAGGTTCCGATGATTAAGGAGGAGGTTCTTT 1842  
OY 1921 TGATGACAAATGACTACTATTATTAACAGACATCAAGGGTACTCTTTCAGTTAGGTGG 1980  
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Db 1843 TCTGACCAATGACTACTTCTTCAAGGACATCAAGGACACCCCTTTCAGTTTGGGGTGG 1902  
OY 1981 CGTTTTCCAGAGGTGATGGAATAATTTCTTCCAGAGGATGTAAACATCGAAGAGCC 2040  
Db 1903 TGTGTCTCCGGGGCAGAGGAATAATATCATCTTCTGTGGGAACACGTCTGTGAAGAGCC 1962  
OY 2041 TGCATGACTTGAACATCCGATGTCTCTTGGAGATGAATGTCTTACTGCAACCTG 2100  
Db 1963 TGCATGACTTCTTCCACCAACCTGAGGCTGAGGCGGGGTGATGATGATGATGATCAG 2022  
OY 2101 ACCTACACCCCTGAGACACCGCATCTGCTCTGATGAAGAGCATTAACCTTACTTAAAG 2160  
Db 2023 ATATTGACCCAGACACCGGAGAGCTCAAGCAGCTGAGAGGCTATGATCCGCTTCTCAACA 2082  
OY 2161 GCAAGAACTCTCTCCAGTGTGATTAAGAAATGTATCAAGAGTCTTCTTTTACCCGG 2220  
Db 2083 GGAAGGACCCAGACCTGAGAGTGTGACAGAGAGCTGTGTCCGGAGAGTGTCTTTTACCCGG 2142  
OY 2221 TGGTGAATGCCCCCATTTGAAGCGTATTTGACACAGCTGGCCCTCAACAAATCTGAAAT 2280  
Db 2143 TGGTGAACAGCCCATGGAAGCTACTGACAGCGCTGAGCCCTCAACATGTCCGAGAGT 2202  
OY 2281 CTGACAAAGGGGTGAGAGTGTCTCTCTGCACTCTGACAGGCGCTCTCCAGATCAACC 2340  
Db 2203 CTGACACAGTGTGTGACATGAGCTCTCTGAGGACCCGCGGTGGCTCTGAGAGAGCT 2262  
OY 2341 TGTGTGTGGGGGTGACAGCTCAACATAGAGACTTCTGAAAGCTGGGAGACAGAGA 2400  
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OY 2401 ACATTTTAAACGACAGACATTTCCCTCTGTGTGACGGAAGAGCCGTGACAGATTCAG 2460  
Db 2323 GCGTGTACACCTTGAGACCGCTGCTCCGCTGTGTGATACCGCAGGCTCAAGACATCTGTG 2382  
OY 2461 GGAGCTTGTCTACTGATCCATTTGACAGCTGGACAGTCA-----ATAAAGCAATG 2514  
Db 2383 GCAAGCTTGTCTTCAACCTCTGCTGGGAGAGAGACCAAGAAATGGCGGGAACCATG 2442  
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OY 2575 CTGTAGGCAATTCAGATGAATCTGAATTTTCCAAAGAAAGTTCTGAGTGCAGAGAC 2634  
Db 2503 CCGCGGCGCTCCAAATGAGCTGGAATTCCTCAAGGCAAAATTTCTGGCGGCAACGG 2562  
OY 2635 AGTGTGCTTCCCTGATGGAATGCTCCATGAGCTGTATGATGAGTGTGAATTTG 2694  
Db 2563 AGTGCAGCACTGTGTGATGGGCGCTGACACAGAGCTGCGAGAGACAGTGTGTGACTGCT 2622  
OY 2695 ACCCTATAGCAATATGATTTATTTTGTGTGTAAGACTATACACAGAGCTGGAGACT 2754  
Db 2623 TCGTATGCAAAACAGGGTTTATCTGTATCTCCAAAGAGTCTCCGAGAGAGGGAAGT 2682  
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OY 2815 GAATTACCTTATGATACCAAGGCAATGTGTAAGGCCAACAGAGAAAGCAGCATGGCG 2874  
Db 2743 AAGTACATATGATATCTATACAGGCAATGTGCAAAACCTCTGAGTACCAACAGTGTGAG 2802  
OY 2875 CCCATGGCTCTCTGATCTTAAATGCTTCTCTGAGTAATAATGATATGATGAGACAG 2934  
Db 2803 CCCAGCCCTGTGTGAGCCCAATTTCTGTCTTGTGACGCGACAGAGTGTGCTGTGAGG 2862  
OY 2935 AACTGTCTTGTCTGTGTGAATTTAACTCTGCAAGTTGTGTGCACTCCGATATGACAG 2994  
Db 2863 AGTGTGTCTGTCTGTGTGAGTGTGTGTGGGCTCTCTGTGACAGAGAGGGCGG 2922  
OY 2995 -----CTAAGCCCAAGAAATTTAAACAGACCTGAGACCTT 3030  
Db 2923 AGGCCAAAGTGTCTTCCATCACTCCCAACAAACAGAAAGACAGACCCGCTGAGACCT 2982



OY	1744	GGCGTGTGTGACGAAAGGAAAAAGGAA---GGAAACCTATATAGTAGCTTGACC	1800
Db	1663	GGCCCTGTACAGAGAGAGGGAAGAACTAAACCCAAACCTATACAAACGTGTGATC	1722
OY	1801	TCTCTGAGGTGAGATGGGAAGACCAGATGACGTGTTGAGAAATGCTATGAGTAATGAA	1860
Db	1723	TCTCGAAGTAGGATGGGAAGACCAAGCTGAATCTCTGAGAACAGCCATGATCAATTAGG	1782
OY	1861	AGACGGGGAAGTTTTCATGAGGTGAAGAAAGACAGTGAGCAAAAGGGAACGGGTTTGG	1920
Db	1783	AAACAGGTACTCTCTCATGGATGTGAAGGTTCCGATGAGTAAAGGAAGGACGATCTCTT	1842
OY	1921	TGATGACAAATGACTACTATTATATACAAACATCAAGGCTACTCCTTTCAGTTAGTGTGG	1980
Db	1843	TCTGTACCAATGACTACTCTTCTTACGGAGATCAACGACACCCCTTTACAGTTTGGGGTGG	1902
OY	1981	CGGTTTCCAGAGGTGATGAGGAAATATTTCTTCGAGGGAATGTAAACATGGAAGAGCC	2040
Db	1903	TGCTGTCCGGGGGCACAGGAATATCAATCTCTTGAGGAAACAGTCTGTGGAAGAGGCC	1962
OY	2041	TGCATGACTTAAACAATCCCGATGTGTCTTGGCAGATGAATGGTCTACTGCAACTG	2100
Db	1963	TGCATGACTTGTTCACCCAGACCTGGCCCTGGCCGGGTGACTGGATCTACTGCATCAG	2022
OY	2101	ACCTACACCTTGAGACCCGCACTCTGTCTAGTTAGAAAGGATTAAGCTTACTTAAAG	2160
Db	2023	ATATTGACCCAGACACACCGAABACTACGCCAGTAAAGGCATATGCTGCTTCCACCA	2082
OY	2161	GCAAGAACCTGTCTCCAGATGTGATTAAGAAATTGATCCAAAGATCTTTTGGACCGG	2220
Db	2083	GGAAGAACCCAGACTGGAGATGTGACGAGAGAGCTGTGCGGGAGGTCTTTTGACCGG	2142
OY	2221	TGCTGAGTGGCCCATTTGAAAGCTATTGGACCAAGCCTGGCCCTCAACAAATCTGAAATT	2280
Db	2143	TGCTGACAGCCCCCATGGAAGCTACTGTGACACCGCTGGCCCTCAACATGTCCGAGAGT	2202
OY	2281	CTGACAAAGGCGTGGAGATTTGCCCTCTGGGCACTGGACAGGGGCTCTCCAGAAATCAC	2340
Db	2203	CTGACACCTGTGTGACATGTGCTTCTGGGCAACCGGCTGGCTCTGGAAGAGAGCT	2262
OY	2341	TGTTTGTGGGGCTGAGCAGCTCACCAATCAGACTTCTGAAAGCTGGCGACAGAGAGA	2400
Db	2263	TGTTCTGTGGGCTCCGAGAAAGTGTCCGACAGGAAGTTCTGTACACCTGTAGAGAGAGCCA	2322
OY	2401	ACATTTTAAACGACACCAATTTCCCTCTCTGTGTAACCGAAGGCGGTGACAGATTCCAG	2460
Db	2323	GGGTGTTCACCTGTGACCCCTTCCGCTGTGTGTAACCGCAGGCTCAGAGCATCTGTGT	2382
OY	2461	GGAGCTGTCTACTGATGCCATTCGACATGAGCACTGACACTCA-----ATTAAGCAATG	2514
Db	2383	GCAGCTTCTCTTCAACCTCCGCTGGGCAAGAAAGGACAAAGATGCGGGGTGAACCATATG	2442
OY	2515	TGGTGAACAGCAATACATCCATCCAGCTCTGGATATGAAGGAATCTCTGTGGTGGCAG	2574
Db	2443	TGGTGAACGCAAGCAGAGCTGTGGGGGTGACCGTGAACAAAGAGCAGCATTTGCTGCAG	2502
OY	2575	CTGTAGGCATTAGATGAATCTTGAATTTTTCCAAAGGAAGTTCTGTGACTGCCAGACAG	2634
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OY	2635	AGTGTGTTCCCTGGATGGCAAAATCCCTCATCAGCTGTGTATATAGACTGTGAATTGTT	2694
Db	2563	AGTGCAGCACTGTGATGGGCCCTGCACACAGAGTGGCAGAGCAGTGATTCGGACTGCT	2622
OY	2695	ACCTCATAGACAAATATGATTTTATTTTGTGTCTGAAGACTACACACAGACTGGAGACT	2754
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OY	2755	TTTTTGTGAGATCGAGGAGCTGTGATGAACAAATTGCTAAACATGGGCTCTTTTAAAA	2814
Db	2683	TTTCTGGGGAGGTGATGTGTCTGTCTGACCAACCTGTCTGACATGGGGGTGTTCAACC	2742
OY	2815	GAATTACCTTTATGACTACCAAGCATGTGTAGAGCCAAACAGGAAGACAGCATGGCG	2874

Db	2743	AGTACACTATGATGACATACAGGCCCATGCGAAACCCCTGAGTCACACACACAGTGCAG	28020
Oy	2875	CCCATGGCCCTCTGGATGCTTATTAATCCCTCTCTCTGCTACATAAATGGATGATGACAG	29334
Db	2803	CCCAAGCCCCCTGGTACAGCCCAATTTCTGCTCTTGACGGCGACCAAGTGGCTGTCAGG	28622
Oy	2935	AACTTGCTTGTCTCTGGTGGAAATTTAACTCTGCAAGTTGTGGCACTCCGATATGACAG	29944
Db	2863	AGCTGTCTCTTCTCTGCTGGAGTGGAGTGTCTGGGGCTCTCTGTGACGACAGAGGGCGG	29222
Oy	2995	-----CTAAGCCAGAAATTTGAACAGACCCCTGAGCCTT	30350
Db	2923	AGGCCAAAAGTGTCTTCATCACTCCACAAACACAAAGACGAGGACCCGCTGACGCCCT	29882
Oy	3031	GTGATACAGGATATACGACATTTGCTGTCTGAGGGCACATCAAGAGACTACAGGGAATA	30980
Db	2993	GCGACACGGAATACCCGTTGTTGTGTACACAGCGGGCCATCTCGGAGAGGCCAAGCGGATCG	30422
Oy	3091	TTGCTTGTGAAGACTGTCTCCAAAGTCTTTGTATCCAGCAAGAAATCCAGACGAAACCTGT	31500
Db	3043	TGGAGTGGGGCCCTGCGCAAAAGTATTTGTGTGTGACAGAAATTTCCCAACAGTAACCTCC	31020
Oy	3151	TCATGTGTGTGTGTGGACAGCAGCAGCTGCTGTGTGAATCTGTGGCCCCATCAACATGGCAC	32100
Db	3103	TCTCTCTGTGTGACAGACCCCACTCTGACACTGCGACGATCTTCCACACAGTGTGACGAGG	31622
Oy	3211	CCATTGAATACGAGTAAATGAATGCCCTTAAGCTGAAGACG	32500
Db	3153	CGACAGAAATCAATTAATTAAGCTCTGTCAAAATGTGACCG	32020

Search completed: April 27, 2003, 23:59:49  
Job time : 9364 secs

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2003, 20:10:56 ; Search time 4606 Seconds  
(without alignments)  
13255.967 Million cell updates/sec

Title: US-09-787-657-3

Perfect score: 3770

Sequence: 1 tactatagggccgcgcga.....aaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32:08132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estlum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estcpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rnd:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	784.8	20.8	880	13	BI915864
3	784.2	20.8	798	12	BG206136
4	688.8	18.3	738	10	AV723130
5	647.2	17.2	818	12	BE740459
6	633.4	16.8	801	12	BG213431

7	583.8	15.5	608	10	AV722352	AV722352
8	561.2	14.9	762	12 <td>BG218214<td>BG218214</td></td>	BG218214 <td>BG218214</td>	BG218214
9	543	14.4	644	14 <td>BM922229<td>BM922229</td></td>	BM922229 <td>BM922229</td>	BM922229
10	523.4	13.9	658	14 <td>BQ329542<td>BQ329542</td></td>	BQ329542 <td>BQ329542</td>	BQ329542
11	518.4	13.8	799	13 <td>BI736456<td>BI736456</td></td>	BI736456 <td>BI736456</td>	BI736456
12	515	13.7	671	12 <td>BE985092<td>BE985092</td></td>	BE985092 <td>BE985092</td>	BE985092
13	500.6	13.3	618	14 <td>BM949850<td>BM949850</td></td>	BM949850 <td>BM949850</td>	BM949850
14	492.4	13.1	711	13 <td>BI736450<td>BI736450</td></td>	BI736450 <td>BI736450</td>	BI736450
15	479.4	12.7	589	12 <td>BE65072<td>BE65072</td></td>	BE65072 <td>BE65072</td>	BE65072
16	458	12.1	505	12 <td>BE924114<td>BE924114</td></td>	BE924114 <td>BE924114</td>	BE924114
17	448.8	11.9	570	9 <td>AI928328<td>AI928328</td></td>	AI928328 <td>AI928328</td>	AI928328
18	447.2	11.9	570	10 <td>AM299346<td>AM299346</td></td>	AM299346 <td>AM299346</td>	AM299346
19	432.4	11.5	843	13 <td>BI732344<td>BI732344</td></td>	BI732344 <td>BI732344</td>	BI732344
20	432.2	11.5	782	12 <td>BE958545<td>BE958545</td></td>	BE958545 <td>BE958545</td>	BE958545
21	431.4	11.4	533	12 <td>BE949415<td>BE949415</td></td>	BE949415 <td>BE949415</td>	BE949415
22	420	11.1	420	9 <td>AI860300<td>AI860300</td></td>	AI860300 <td>AI860300</td>	AI860300
23	419	11.1	492	9 <td>AA188635<td>AA188635</td></td>	AA188635 <td>AA188635</td>	AA188635
24	414.8	11.0	628	13 <td>BM114312<td>BM114312</td></td>	BM114312 <td>BM114312</td>	BM114312
25	405.2	10.7	551	10 <td>AM655372<td>AM655372</td></td>	AM655372 <td>AM655372</td>	AM655372
26	404.4	10.7	502	10 <td>AM491939<td>AM491939</td></td>	AM491939 <td>AM491939</td>	AM491939
27	401.4	10.6	450	9 <td>AI290166<td>AI290166</td></td>	AI290166 <td>AI290166</td>	AI290166
28	392.8	10.4	408	12 <td>BE768630<td>BE768630</td></td>	BE768630 <td>BE768630</td>	BE768630
29	382.6	10.1	405	14 <td>BQ340959<td>BQ340959</td></td>	BQ340959 <td>BQ340959</td>	BQ340959
30	369.6	9.8	509	9 <td>AA190607<td>AA190607</td></td>	AA190607 <td>AA190607</td>	AA190607
31	363.4	9.6	365	12 <td>BE711310<td>BE711310</td></td>	BE711310 <td>BE711310</td>	BE711310
32	361.8	9.6	365	12 <td>BE702896<td>BE702896</td></td>	BE702896 <td>BE702896</td>	BE702896
33	361.8	9.6	365	12 <td>BE702897<td>BE702897</td></td>	BE702897 <td>BE702897</td>	BE702897
34	361.8	9.6	365	12 <td>BE764531<td>BE764531</td></td>	BE764531 <td>BE764531</td>	BE764531
35	361.2	9.6	381	12 <td>BE702863<td>BE702863</td></td>	BE702863 <td>BE702863</td>	BE702863
36	359.2	9.5	364	12 <td>BF943019<td>BF943019</td></td>	BF943019 <td>BF943019</td>	BF943019
37	358.6	9.5	365	13 <td>BI035064<td>BI035064</td></td>	BI035064 <td>BI035064</td>	BI035064
38	356	9.4	462	14 <td>R20288<td>R20288</td></td>	R20288 <td>R20288</td>	R20288
39	354.2	9.4	421	9 <td>AI624354<td>AI624354</td></td>	AI624354 <td>AI624354</td>	AI624354
40	344	9.1	357	10 <td>AM014849<td>AM014849</td></td>	AM014849 <td>AM014849</td>	AM014849
41	343.4	9.1	357	12 <td>BE768691<td>BE768691</td></td>	BE768691 <td>BE768691</td>	BE768691
42	339	9.0	340	14	244942 <td>244942</td>	244942
43	330.6	8.8	428	9 <td>AA815447<td>AA815447</td></td>	AA815447 <td>AA815447</td>	AA815447
44	328.8	8.7	332	12 <td>BE768727<td>BE768727</td></td>	BE768727 <td>BE768727</td>	BE768727
45	328.2	8.7	365	12 <td>BF364499<td>BF364499</td></td>	BF364499 <td>BF364499</td>	BF364499

#### ALIGNMENTS

RESULT 1  
BI753834

LOCUS 603027515F1 NTH\_MGC\_114 Homo sapiens cdna clone IMAGE:5198015 5',  
DEFINITION mRNA sequence.

ACCESSION BI753834.1 GI:15745412

VERSION BI753834.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 966)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cga@pds-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM11495 row: n column: 04

High quality sequence stop: 784.

Location/Qualifiers

1..966

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5198019"
/clone_1lb="NIH_MGC_114"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library."
BASE COUNT      258 a      221 c      234 g      251 t      2 others
ORIGIN

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Query Match      21.6% Score 813; DB 13; Length 966;
Best Local Similarity 94.3%; Pred. No. 2,1e-130;
Matches 919; Conservative 0; Mismatches 47; Indels 9; Gaps 7;

QY 2526 AGTACATCATCCAGCTCTGATGAGGAATCTCTGTGTGGCAGCTGTAGCAATT 2585
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Db 1 AGTACATCATCCAGCTCTGATGAGGAATCTCTGTGTGGCAGCTGTAGCAATT 60

QY 2386 CAGATGAACCTGAAATTTTCCAAAGAGAGTCTGACAGCAGACAGAGTCTTCC 2645
    |||||||
Db 61 CAGATGAACCTGAAATTTTCCAAAGAGAGTCTGACAGCAGACAGAGTCTTCC 120

QY 2646 CTGATGAGCAATGCTCATGAGTGTATGATAGAGCTGTAATTTGTACCTATAGAC 2705
    |||||||
Db 121 CTGATGAGCAATGCTCATGAGTGTATGATAGAGCTGTAATTTGTACCTATAGAC 180

QY 2706 AATTAATGATTTATTTTGGTGTCTGAAGACACACAGAGTGTAGAGCTTTTGGTGAG 2765
    |||||||
Db 181 AATTAATGATTTATTTTGGTGTCTGAAGACACACAGAGTGTAGAGCTTTTGGTGAG 240

QY 2766 ATCGAGGAGCTGTATGAGCAATGCTTAACATGGGCTCTTAAAGAAATTAACCTT 2825
    |||||||
Db 241 ATCGAGGAGCTGTATGAGCAATGCTTAACATGGGCTCTTAAAGAAATTAACCTT 300

QY 2826 TATGACACCAAGCAGTGTAGAGCCACCAAGAGAGAGAGGCGCCATGGCCTC 2885
    |||||||
Db 301 TATGACACCAAGCAGTGTAGAGCCACCAAGAGAGAGAGGCGCCATGGCCTC 360

QY 2886 CTGATGCTTATATGCTCTCTCTGAGTAAATGATGATGATGATGATGATGATGATG 2945
    |||||||
Db 361 CTGATGCTTATATGCTCTCTCTCTGAGTAAATGATGATGATGATGATGATGATGATG 420

QY 2946 TTTCTGCTGGAATTTAACTCTGACAGTTGGTGGCAGCTCCGATATGACAGTAAAGCCAG 3005
    |||||||
Db 421 TTTCTGCTGGAATTTAACTCTGACAGTTGGTGGCAGCTCCGATATGACAGTAAAGCCAG 480

QY 3006 AATTTGAACAGAGCCTGGAGAGCTTTGATAGTATTCACAGATTCCTCTGAGCCG 3065
    |||||||
Db 481 AATTTGAACAGAGCCTGGAGAGCTTTGATAGTATTCACAGATTCCTCTGAGCCG 540

QY 3066 ACCATCAAGAGAGCTACAGAGGAATTTGCTGTGAAGAGCTCTCCCAAGTCTTTGATATC 3125
    |||||||
Db 541 ACCATCAAGAGAGCTACAGAGGAATTTGCTGTGAAGAGCTCTCCCAAGTCTTTGATATC 599

QY 3126 CAGCAAAATCCCAAGAGAGCAATCTTTGATGAGTGTGGTGGAGAGAGTGGCTCTGTGAA 3185
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Db 600 CAGCAAAATCCCAAGAGAGCAATCTTTGATGAGTGTGGTGGAGAGAGTGGCTCTGTGAA 659

QY 3186 TCTGTGGCCCATCATCAGTGTGACCCATTTGAATTCAGTATTAATGATCCCTTAAGTGT 3245
    |||||||
Db 660 TCTGTGGCCCATCATCAGTGTGACCCATTTGAATTCAGTATTAATGATCCCTTAAGTGT 719

QY 3246 GAACGCTTAAGAGCCAGAAATGAGAGGCGCCAGAAATCTTTGATGAGCTTCACTCT 3305
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Db 720 GAACGCTTAAGAG -CCAGAAATGAGAGGCGCCAGAAATCTTTGATGAGCTTCACTCT 776

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QY 3306 GAGGAGAAATGCAAGGAGCTGTGGGGTGGCGCCGAGTCTCCAGCCAGACAGTCTCTCT 3365
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Db 777 GAGGAGAAATGCAAGGAGCTGTGGGGTGGCGGAGAGTCTCC -AGCCAGAGACAGTCTCTCT 835

QY 3366 CTGTCGCCCTCTGCTTTGATGCTCTTCAAGGTACAGTACAGTACAGTGTCTCTACT 3425
    |||||||
Db 836 TCTGTCCCTCTG -GTTTGAATGCTCTTCAAGGTACAGTACAGTACAGTGTCTCTACT 894

QY 3426 GACTGAGATGTCTCTTGGCATCTAAATCATGATGATTAACATGTGAACCAATATATGTGC 3485
    |||||||
Db 895 GACTGAAATGT -TCTCTGGAGTGGTTAATCATAG -TAACTGTGAACCAATATGTGGGCAC 951

QY 3486 AATCATCAGACATG 3500
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Db 952 TACACACCTGAATG 966

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RESULT 2
LOCUS      B1915864      880 bp      mRNA      linear      EST 16-OCT-2001
DEFINITION 603184526F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248447 5',
            mRNA sequence.
ACCESSION  B1915864
VERSION    B1915864.1 GI:16179807
KEYWORDS  EST.
SOURCE     human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 880)
            NIH-MGC http://mgc.ncl.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            Plate: LLMH1627 row: c column: 08
            High quality sequence stop: 740.
            Location/Qualifiers
                1..880
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5248447"
                /clone_1lb="NIH_MGC_121"
                /lab_host="DH10B"
                /Note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."
BASE COUNT      257 a      221 c      175 g      227 t
ORIGIN

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Query Match      20.8% Score 784.8; DB 13; Length 880;
Best Local Similarity 96.6%; Pred. No. 1.6e-125;
Matches 823; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

QY 2921 ATGATCATGACAGAACTGTCTTCTGCTGGAATTTAACTCTGACATGGTGCA 2980
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Db 1 ATGATCATGACAGAACTGTCTTCTGCTGGAATTTAACTCTGACATGGTGCA 60

QY 2981 CTGCGATATGACAGCTTAAGCCCAAGAAATGAACAGACAGCCTGAGCCTTGTGATACTGA 3040

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[illegible]

TITLE	Creation of genome-wide protein expression libraries using random
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE	21227151
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: <a href="mailto:scaine@athersys.com">scaine@athersys.com</a> High quality sequence stop: 551.
FEATURES	Location/Qualifiers
Source	1. .798 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="H1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."
BASE COUNT	215 a 196 c 178 g 209 t
ORIGIN	
Query Match	20.8%; Score 784.2; DB 12; Length 798;
Best Local Similarity	99.0%; Pred No.2e-125;
Matches 789: Conservative	0; Mismatches 8; Indels 0; Gaps 0
OY 2822	CCTTTATGACTACCAAGCCATGTGTAGACCACCAAGAAAGCAGCGATGGCCCATGG 2881
Db 1	CCTTATGACTACCATGCATGTGTAGACCACCAAGAAAGCAGCGATGGCCCATGG 60
OY 2882	CCTCCTGCATCCTTTATATGCCCTTCTCTCTGCAGTAAATAGATCATACAGACTTGT 2941
Db 61	CCTCCTGCATCCTTTATATGCCCTTCTCTCTGCAGTAAATAGATCATACAGAACTTGT 120
OY 2942	CTTGTTCCTGGGGAATTTAACCTTGCAGTTGGTGGCACTCGATATGACAGCTTAAGC 3001
Db 121	CTTGTTCCTGGGGAATTTAACCTTGCAGTTGGTGGCACTCGATATGACAGCTTAAGC 180
OY 3002	CCAGAAATTTGAACAGACCCTGGAGCCTTGATATCTGATATTCAGATTCGATGCTCTGA 3061
Db 181	CCAGAAATTTGAACAGACCCTGGAGCCTTGATATCTGATATTCAGATTCGATGCTCTGA 240
OY 3062	GGCACCATCAAGAGACTACAGGGAATTTGCTTGTGAAGACTGCTCCAACTCTTTGT 3121
Db 241	GGCACCATCAAGAGACTACAGGGAATTTGCTTGTGAAGACTGCTCCAACTCTTTGT 300
OY 3122	CATTCAGCAAAATCCCAAGCAGCAACCTGTTCAATGTGTGGTGGAGACAGAGCTGCCTTG 3181
Db 301	CATTCAGCAAAATCCCAAGCAGCAACCTGTTCAATGTGTGGTGGAGACAGAGCTGCCTTG 360
OY 3182	TGAATCTGGGCCCATATCACCATGCACCACTTGAATCAGATTAATGAATTCCTTAA 3241
Db 361	TGAATCTGGGCCCATATCACCATGCACCACTTGAATCAGATTAATGAATTCCTTAA 420
OY 3242	GTGTGAACGCTTAAAGGCCCAGAAATCAGAAGGGGCCCGAGATCTTGTATGGCTTCA 3301
Db 421	GTGTGAACGCTTAAAGGCCCAGAAATCAGAAGGGGCCCGAGATCTTGTATGGCTTCA 480
OY 3302	TCCTAGAGAAATGCAAGGGAATGTGGGGGTGCGCCGAATCTTCCAAAGCCCAAGACATCT 3361
Db 481	TCCTAGAGAGAAATGCAAGGGAATGTGGGGGTGCGCCGAATCTTCCAAAGCCCAAGACATCT 540
OY 3362	CCTTGTGCCCTCTGCTTTTATCTCTCTTCCAAAGGTACACTGATAGATGTTCTCT 3421
Db 541	CCTTGTGCCCTCTGCTTTTATCTCTCTTCCAAAGGTACACTGATAGATGTTCTCT 600
OY 3422	TACTGACTGAGATGTTCTTGTGGATGCTAAATCATGTAGATAAATCTGAACCAATAATG 3481
Db 601	TACTGACTGAGATGTTCTTGTGGATGCTAAATCATGTAGATAAATCTGAACCAATAATG 660

QY 3482 GTGCAACATAGACATGATATATGTCACACATCCTCATCATGATTTAACT 3541  
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Db 661 GTGCAACATAGACATGATATATGTCACACATCCTCATCATGATTTAACT 720  
QY 3542 GTGCGTATATTAACCTTTAAAGATATGTTGACAAAAGTTATCATCTTTTACTT 3601  
|||||  
Db 721 GTGCGTATATTAACCTTTAAAGATATGTTGACAAAAGTTATCATCTTTTACTT 780  
QY 3602 TGGCAGTCATGCAATG 3618  
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Db 781 TGGCAGTCATGCAATG 797

RESULT 4  
AV723130 738 bp mRNA linear EST 16-OCT-2000  
LOCUS AV723130 HNB Homo sapiens cDNA clone HTBAPB04 5', mRNA sequence.  
ACCESSION AV723130  
VERSION AV723130.1 GI:10826300  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 738)  
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,  
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu,  
Shen, J., Chen, Z., and Han, Z.  
Chen, J., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,  
Homo sapiens cDNA HNB clones  
Unpublished (2000)  
TITLE Chinese National Human Genome Center at Shanghai  
JOURNAL 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
COMMENT Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
Source Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="HTBAPB04"  
/tissue="Hypothalamus"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 196 a 182 c 180 g 180 t  
ORIGIN

Query Match 18.3%; Score 688.8; DB 10; Length 738;  
Best Local Similarity 97.7%; Pred. No. 5.7e-109;  
Matches 721; Conservative 0; Mismatches 12; Indels 5; Gaps 2;

QY 2072 GGCAGATTAATGCTCTACTGACACAGTACACCTGAGACCGCCATCTCTCA 2131  
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Db 1 GGCAGATTAATGCTCTACTGACACAGTACACCTGAGACCGCCATCTCTCA 60  
QY 2132 GTTAAAGCGATTAAGCTCTAAAGGCAAAAGAACCTCTGCTCCAGTGTATGAAGA 2191  
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Db 61 GTTAAAGCGATTAAGCTCTAAAGGCAAAAGAACCTCTGCTCCAGTGTATGAAGA 120  
QY 2192 ATTGATCCAAAGATCTTTTGAACGCGGTGAGTGCCTCCCATTTGAAGGATTTGAC 2251  
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Db 121 ATTGATCCAAAGATCTTTTGAACGCGGTGAGTGCCTCCCATTTGAAGGATTTGAC 180  
QY 2252 CAGCGTGGCCCTCAACAATCTGAAATTTCTGACAAAGGCGTGGAGGTTCCCTTCGCG 2311  
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Db 181 CAGCGTGGCCCTCAACAATCTGAAATTTCTGACAAAGGCGTGGAGGTTCCCTTCGCG 240

QY 2312 CACTCGCAGCGGCTCTCTCAGATCAACCTGTTTTCGGGCTGAGAGCTCACCAATCA 2371  
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Db 241 CACTCGCAGCGGCTCTCTCAGATCAACCTGTTTTCGGGCTGAGAGCTCACCAATCA 300  
QY 2372 GCAGCTCTGAAAGCTGGCGACAAAGAGAACATTTTAAAGCAGACATTTCCCTCTCG 2431  
|||||  
Db 301 GCAGCTCTGAAAGCTGGCGACAAAGAGAACATTTTAAAGCAGACATTTCCCTCTCG 360  
QY 2432 GTACGGAAGACCGCTGAGAGATTCAGAGGCTGCTGCTACCTGATCCATCCATCAGAC 2491  
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Db 361 GTACGGAAGACCGCTGAGAGATTCAGAGGCTGCTGCTACCTGATCCATCCATCAGAC 420  
QY 2492 TGAACAGTCAATTAAGCAATGTGTGACAGCAAGTACATCCATCCATCCATCCATCA 2551  
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Db 421 TGAACAGTCAATTAAGCAATGTGTGACAGCAAGTACATCCATCCATCCATCCATCA 480  
QY 2552 ACGGAATCTCTCTGCTGCTGAGCTGTAGGCTATGAGTGAATTTTCCAAAG 2611  
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Db 481 ACGGAATCTCTCTGCTGCTGAGCTGTAGGCTATGAGTGAATTTTCCAAAG 540  
QY 2612 GAAGTCTGACGCTGACAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2671  
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Db 541 GATGTTCTGACGCTGACAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
QY 2672 TGATGATGAGACTGTGAATTTTACCTCATATAGCAATATGATTTTGTGCTGTA 2731  
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Db 601 TGATGATGAGACTGTGAATTTTACCTCATATAGCAATATGATTTTGTGCTGTA 659  
QY 2732 AGACTACACACAGCTGAGAGCTTTTGTGAGTGAAGGAGCTGTGTAACAAT 2791  
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Db 660 AGACTACACACAGCTGAGAGCTTTTGTGAGTGAAGGAGCTGTGTAACAAT 715  
QY 2792 GCTAACATGGCTCCTT 2809  
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Db 716 GCTAACATGGCTCCTT 733

RESULT 5  
BE740459 818 bp mRNA linear EST 15-SEP-2000  
LOCUS BE740459  
DEFINITION 601595508F1 NIH\_MGC\_9 Homo sapiens cDNA clone IMAGE:3949657 5',  
mRNA sequence.  
ACCESSION BE740459  
VERSION BE740459.1 GI:10154451  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 818)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at: Image.lnl.gov  
Plate: L1CM814 row: 0 column: 02  
High quality sequence stop: 774.

FEATURES  
Source Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:3949657"  
/clone="NIH\_MGC\_9"  
/tissue="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: ovary; Vector: pOTB7; Site\_1: XhoI; Site\_2:



ECORI: cDNA made by oligo-dT priming. Directionally cloned into EcorI/XhoI sites using the following 5' adaptor: GGACGAG(g). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 244 a 169 c 205 g 200 t

Query Match 17.2%; Score 647.2; DB 12; Length 818;  
Best Local Similarity 89.4%; Pred. No. 8.2e-102;  
Matches 794; Conservative 1; Mismatches 14; Indels 79; Gaps 6;

QY 954 CGCTGACTATCGGAGCAACAGCTCATCATTTTGGATACCTTGGAGATGAC 1013  
DB 1 CGCTGACTATCGGAGCAACAGCTCATCATTTTGGATACCTTGGAGATGAC 60  
QY 1014 TTCTTCAACATATGCTTATATGAGAGCTTCACTATGTGAACTTGGCTGAATGA 1073  
DB 61 TTCTTCAACATATGCTTATATGAGAGCTTCACTATGTGAACTTGGCTGAATGA 120  
QY 1074 ACTTGGTGAAGCCGACAGACAAAGAGCCTTCAAGGAGCATTTGGAGAACTT 1133  
DB 121 ACTTGGTGAAGCCGACAGACAAAGAGCCTTCAAGGAGCATTTGGAGAACTT 180  
QY 1134 TTGCGCAAGAAATTTGGAATTTGGATATAGCTCTGATGAGAGCTTCAACATCTGAGT 1193  
DB 181 TTGCGCAAGAAATTTGGAATTTGGATATAGCTCTGATGAGAGCTTCAACATCTGAGT 240  
QY 1194 GATTTCACACAGGAGCAAGAGATATGTCAGTCAGGACCATCATGCTCATTAACATGAT 1253  
DB 241 GATTTCACACAGGAGCAAGAGATATGTCAGTCAGGACCATCATGCTCATTAACATGAT 300  
QY 1254 GGGGCGGTGACACCTTATGATATCTTTGCAAAATATCAATTTGGCAATTCGAAAGATT 1313  
DB 301 GGGGCGGTGACACCTTATGATATCTTTGCAAAATATCAATTTGGCAATTCGAAAGATT 360  
QY 1314 CGCATCTTCACATACCTTATGAGAGAGCTGCGTTTGCAGCAATTTAAAGTGGATG 1373  
DB 361 CGCATCTTCACATACCTTATGAGAGAGCTGCGTTTGCAGCAATTTAAAGTGGATG 420  
QY 1374 GCGTGGCCCAAGAGATTTTACCAGATCTCCACTTGGCTGATTTGCAAGAGAT 1433  
DB 421 GCGTGGCCCAAGAGATTTTACCAGATCTCCACTTGGCTGATTTGCAAGAGAT 480  
QY 1434 GTCATGGAATACCTTACGCTTATAGCGGCGCAAGATCATACCAAGAGATGATG 1493  
DB 481 GTCATGGAATACCTTACGCTTATAGCGGCGCAAGATCATACCAAGAGATGATG 539  
QY 1494 GTGTGGACCGAAGCTTACATTTGACAGCACTCTGATGATGATCAGGCGCCGTCCTGATG 1553  
DB 540 GTGTGGACCGAAGCTTACATTTGACAGCACTCTGATGATGATCAGGCGCCGTCCTGATG 569  
QY 1554 ACCACGTGAGCCATGCTGCTGTTTAAAGACAGCAAGCAAGATCGAAGGCAATTTCTT 1613  
DB 570 -----AGATCGAAGGCAATTTCTT 587  
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DB 588 CTGGAGATGTTGGACAGATGTCAGTGAAGAACTTCTGAAGACCTTCCCAATATAC 647  
QY 1674 AAGTTAGGATTCACGCTTATGCTTGGCAATCACAATATGATGATATAT -CTGAGAGCAT 1733  
DB 648 AAGTTAGGATTCACGCTTATGCTTGGCAATCACAATATGATGATATAT -CTGAGAGCAT 706  
QY 1734 CCGGAACCTAGGCTGCTGTACAGAAAGAAAGAGCAAGCAACTTACTATAGTAC 1793  
DB 707 CCGGAACCTAGGCTGCTGTACAGAAAGAAAGAGCAAGCAACTTACTATAGTAC --CTAATATAGTA -- 762  
QY 1794 GTTGAACCTCTGAGGTGAGTGGAGCAAGCAAGATGATGATGTTGAGA 1841  
DB 763 CATTGACTCTCTGAGGTGAGTGGAGCAAGCAAGATGATGATGTTGAGA 809

RESULT 6  
BG213431  
LOCUS  
DEFINITION  
R5733037 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
VERSION  
BG213431  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 801)  
AUTHORS  
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,  
Leiner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,  
J., Danzig,J., and Ducar,M.  
J., Danzig,J., and Ducar,M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
TITLE  
Net. Biotechnol. 19 (5), 440-445 (2001)  
JOURNAL  
MEDLINE  
21227151  
COMMENT  
Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atersys.com  
High quality sequence stop: 477.  
location/qualifiers  
1. 801  
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/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 221 a 191 c 183 g 205 t 1 others

ORIGIN

Query Match 16.8%; Score 633.4; DB 12; Length 801;  
Best Local Similarity 91.3%; Pred. No. 2e-99;  
Matches 723; Conservative 0; Mismatches 22; Indels 47; Gaps 3;

QY 2688 AATTGTACCTATAGCAATTAATGATTTATTTGGTGTGTAAGCTACACAGACT 2747  
DB 13 AATTGTACCTATAGCAATTAATGATTTATTTGGTGTGTAAGCTACACAGACT 72  
QY 2748 GGAGACTTTTGGTGTGATCGAGGAGAGCTGTGATGAACAAATTTGCTAAAGGGCTCC 2807  
DB 73 GGAGACTTTTGGTGTGATCGAGGAGAGCTGTGATGAACAAATTTGCTAAAGGGCTCC 132  
QY 2808 TTTAAAAAATTAACCTTTATGACATCAAGCCATGTGTAGAGCAACAAAGAAAGCAGC 2867  
DB 133 TTTAAAAAATTAACCTTTATGACATCAAGCCATGTGTAGAGCAACAAAGAAAGCAGC 192  
QY 2868 GATGGGCGCCATGAGCTCCGATGCTTTAATGAGCTTCTCTGAGTAAATGATGAT 2927  
DB 193 GATGGGCGCCATGAGCTCCGATGCTTTAATGAGCTTCTCTGAGTAAATGATGAT 252  
QY 2928 ATGACAGAACTTGTCTTGTCTGTGATGATTTAACTCTGAGTGTGAGCACTCCGAT 2987  
DB 253 ATGACAGAACTTGTCTTGTCTGTGATGATTTAACTCTGAGTGTGAGCACTCCGAT 312  
QY 2988 ATGACAGCTTAAAGCCGAGAAATTTGAACAGACCTTGAGCTTTGTGATATCTGATCA 3047  
DB 313 ATGACAGCTTAAAGCCGAGAAATTTGAACAGACCTTGAGCTTTGTGATATCTGATCA 372

QY 3048 GCATTCGTCTGTGAGCGGACCATCAAGAGACTACAGGGAATATTGCTTGTGAAGACTGC 3107  
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Db 373 GCATTCGTCTGTGAGCGGACCATCAAGAGACTACAGGGAATATTGCTTGTGAAGACTGC 432  
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QY 3108 TCCAGTCTTGTGATCCAGCAATCCCAAGCAGCAACCTGTTGATGCTGTGTGAC 3167  
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Db 433 TCCAGTCTTGTGATCCAGCAATCCCAAGCAGCAACCTGTTGATGCTGTGTGAC 492  
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QY 3168 AGCAGCTCTGTGATCTGTGCGCCCATCAACAGTGGACCCCATTTGAATGAC----- 3223  
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Db 493 AGCAGCTCTGTGATCTGTGCGCCCATCAACAGTGGACCCCATTTGAATGACAGATA 552  
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QY 3224 -----GTATATGATCCCTTAAGT 3243  
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Db 553 GAAAAAGCAATCCCTGGAAACATGCTTAACTACAGTCAACATATGATATCCCTTAAGT 612  
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QY 3244 GTGAAGCTTAAAGCCCAAGAGATCAGAGCGCCCAAGATCTTGTGATGCTTTCATC 3303  
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Db 613 GTGAAGCTTAAAGCCCAAGAGATCAGAGCGCCCAAGATCTTGTGATGCTTTCATC 672  
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QY 3304 CTGAGGAATGCAAGGAGTGTGGGGTGGCGGAGTCTCCAGCCAGACAGCTCC 3363  
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QY 3364 TTCTGCTCCCTGCTTGTGATGCTTCTCAAGTGAAGTGAAGTGAAGTCTTCTTA 3423  
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QY 3424 CTGACTGAGATG 3435  
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Db 790 CTGACTGAGATG 801  
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RESULT 7  
AV722352 608 bp mRNA linear EST 16-OCT-2000  
LOCUS AV722352 HTB Homo sapiens cDNA clone HTBAVB10 5', mRNA sequence.  
DEFINITION AV722352  
VERSION AV722352.1 GI:10824752  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 608)  
Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,  
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,  
S., Gu,W., Tu,Y., Jia,D., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,  
Chen,J., Chen,Z. and Han,Z.  
Homo sapiens cDNA HTB clones  
Unpublished (2000)  
CONTACT: Zenguan Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@hgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
Source location/Qualifiers  
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/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 159 a 150 c 141 g 157 t 1 others  
ORIGIN

Query Match 15.5% Score 583.8; DB 10; Length 608;  
Best Local Similarity 98.8%; Pred. No. 7.5e-91;  
Matches 599; Conservative 0; Mismatches 3; Indels 4; Gaps 1;  
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Db 1 GTGGAATTTAACTTGTGAGTGGGACATCCGATATGACAGCTAAAGCCAGAAATTTG 60  
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QY 3012 AAACAGACCTTGAGACCTTGTGATAGTAATATTCAGATTCGCTGTGAGCGACATC 3071  
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Db 61 AAACAGACCTTGAGACCTTGTGATAGTAATATTCAGATTCGCTGTGAGCGACATC 120  
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QY 3072 AAGGACTACAGGGAATTTGCTTGTGAAGAGCTCCAGTCTTGTGATCCAGCA 3131  
|||||  
Db 121 AAGGACTACAGGGAATTTGCTTGTGAAGAGCTCCAGTCTTGTGATCCAGCA 180  
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QY 3132 ATCCCAAGCAGCAACCTTGTGATGCTGTGAGACAGACCTGCTTGTGATCTGTG 3191  
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Db 181 ATCCCAAGCAGCAACCTTGTGATGCTGTGAGACAGACCTGCTTGTGATCTGTG 240  
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QY 3192 GCCCCATCACCATGACACCCATTGAATATGATATGATATCCCTTAAGTGAACGT 3251  
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Db 241 GCCCCATCACCATGACACCCATTGAATATGATATGATATCCCTTAAGTGAACGT 300  
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QY 3252 CTAAAGGCCCAAGATCAGAGGCGCCAGAAATCTTGTATGCTTGTGATCTGTGAGAG 3311  
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Db 301 CTAAAGGCCCAAGATCAGAGGCGCCAGAAATCTTGTATGCTTGTGATCTGTGAGAG 360  
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QY 3312 AATCAAGGAGTGTGGGGTGGCGGAGTCTCCAGCCAGACAGTCCCTTCTGCTC 3371  
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Db 361 AATCAAGGAGTGTGGGGTGGCGGAGTCTCCAGCCAGACAGTCCCTTCTGCTC 420  
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QY 3372 CCTGCTTTTGTGATGCTTCTCAAGTGAAGTGAAGTGAAGTCTTCTTACTGATGA 3431  
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Db 421 CCTGCTTTTGTGATGCTTCTCAAGTGAAGTGAAGTGAAGTCTTCTTACTGATGA 480  
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QY 3432 GATGCTCTTGTGATGCTTCAATATGATGATTAAGTGAAGCAAAATATGCTGACATA 3491  
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Db 481 GATGCTCTTGTGATGCTTCAATATGATGATTAAGTGAAGCAAAATATGCTGACATA 536  
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QY 3492 CGAGACATGATATAGTCAACCATCAGATCATCATGATTTAAAGTGGCGATGA 3551  
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Db 537 CGAGACATGATATAGTCAACCATCAGATCATCATGATTTAAAGTGGCGATGA 596  
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Db 597 TAACT 602  
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RESULT 8  
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LOCUS BG218214  
DEFINITION RST37941 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG218214  
VERSION BG218214.1 GI:13744235  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 762)  
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,  
J., Veloso,N., Klika,A., Hess,J., Cothen,K., Lo,K., Offenbacher,  
J., Danzig,J. and Ducar,M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
21227151  
CONTACT: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA



TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202653
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL. (http://www.ludwig.org.br/scripts/gethtml2.pl?tl1=MR4&cl2=MR4-EN0075-220101-006-104&tl3=2001-01-22&cl4=1) Seq primer: puc 18 forward. High quality sequence start: 117 High quality sequence stop: 138. Location/Qualifiers 1..658
FEATURES	
source	

RESULT 11	
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LOCUS	799 bp
DEFINITION	mus musculus cDNA clone IMAGE:5386518 5',
ACCESSION	BI736456
VERSION	BI736456.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
1 (bases 1 to 799)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

FEATURES	SOURCE
Location/Qualifiers	
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/lab_host="DH10B (phage-resistant)"	
/note="Organ: eye; Vector: PCWV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed; Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NIH_MGC library."	
799..1000	

Query Match	13.8%;	Score 518.4;	DB 13;	Length 799;
Best local similarity	86.4%;	Prod No 130-70;		

QY	2736	TACACACAGACTGGAGACTTTTGTGGTAATGAGAGACCTGTGATGAAACAAATTGGTA	279
Db	116	TCCCTACAGACTGGAGATTTTGTGGTAGAGTGGAGAGACTTCTATGAAACAGTTGGTA	175
QY	2736	ACATGGGCTCTTTAAAGAATTAACCTTTATGACTACCAAGCATGTATAGAGCAAC	285
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QY	2856	AAGGAAGCACCAGTATGGCCGCAATGGGCTCTTGATCTTATATGCTTTCTCTGCA	2915
Db	236	AAGGAGACACTGACATGCCCAATGACCTTGACCCCTATTAAGGCTTTCTCTGCA	295
QY	2916	GTAATAATGATCAGACAGAACTGTCTGTGCTGTGGAAATTTAACCTGCGAGTTGG	2975
Db	296	GCCAAAGTGGATTAATGACGGAACTTGTCTGTCTGTGGAGTTTAACCTGTGCAAGTTGG	355
QY	2976	TGGCACTCCGATATGACAGCTAAAGCCAGAAATTTGAAACAGACCTGTGAGCTTGAT	3035
Db	356	TGGCACTCCGACATGACAGCTTAAGCCAGAAATTTGAAACAGACCTGTGAGCTTGAT	415
QY	3036	ACTGAATATCCAGATTTCGTCTGTGAGCGCAACATCAAGAGACTACAGAGAAATTTGCT	3095
Db	416	ACTGAATATCCAGACTTTGTCTGTGAGCGCAACATCAAGAGACTACAGAGAAATTTGCT	475
QY	3096	TGTGAACAGCTGTCAGAGCTTTGTCTGTATCCAGCAAAATCCCAAGCAGCAACTGTTATG	3155
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QY	3156	GTTGTGTGTGACAGACAGCTGCTCTGTGAAATCTGTGGCCCCCATGACAAATGGACCCATT	3215
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QY	3216	GAATATCAGTATTAATGAAATCCCTTAAAGTGAACGCTTAAGAGCCAGAGATCAGAAG	3275
Db	596	GAATATCAGTATTAATGAAATCCCTTAAAGTGAACGCTTAAGAGCTCAGAAGTCAAGAGA	655
QY	3276	CGCCGCAAAATCTGTATGGCTTCCATCCTGAGAGAAATGCCAAGGAGTCTGTGGGGCTCG	3335

Db 656 CGTCCAGATCTCTGCGCAGG-TTCCATCTCAGGAGATGCAAGAGTGTGGGGTGCA 714

QY 3336 CCGAGTCTTCCAGGCCCAAGACAGTCTCTCTCTGCTGCCCTGCTTTTGATGCTTCTTCA 339

Db 715 TCGAGTCTTTCAGGCCCAAGAGCGGGCTTCTGCTGCTGCCCTGTTGAGTCTCTTCTCA 774

QY 3396 AGGTGACACACTGATGA 3411

Db 775 AGGTGACACTAATTA 790

RESULT	12
BE985092	
LOCUS	671 bp mRNA linear EST 29-APR-2002
DEFINITION	U1-M-CG0P-bdh-c-10-0-U1.s1 NIH_BMAP_RetL_S2 Mus musculus cDNA clone.
ACCESSION	BE985092
VERSION	BE985092.1 GI:10658046
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

oligo-dT track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialised non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The cDNA for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine The following repetitive elements were found in this cDNA sequence: 3-35, >(CGG)n#Simple\_repeat  
Seq primer: M13 Forward  
POLYA-No.

ORIGIN	BASE COUNT	Query Match	Best Local Similarity
<pre> /organism="Mus musculus" /strain="C57BL/6Jr" /db_xref="taxon:10090" /clone="UI-M-G0P-bdh-c-10-0-0i" /clone_11b="NIH_BMAP_Ret4_S2" /lab_host="DH10B (Life Technologies)" /note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainrest.eng.utoro.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine TAG_SEQ=None found" </pre>	160 a 164 c 194 g 152 t 1 others	13.7%; Score 515; DB 12; Length 671;	87.8%; Pred. No. 5,2e-79;



OY 2180 GTGTGATTAAGAAATTCACAGAGAGTCTTTTGTAGCGGTGGTGAAGGCCCATTTGA 2239  
 Db 540 ATGTGACAAAGAAATTTGATCANGAAGTCTTTTGTAGCTGTGTGTGAGCGCCCATTTGA 599  
 OY 2240 AGCGTATTGGACCGCCTG 2258  
 Db 600 AGCCTATTGGACGAGCCTG 618  
 RESULT 14  
 B1736450 711 bp mRNA linear EST 20-SEP-2001  
 B1736450 603359485F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5366516 5',  
 mRNA sequence.  
 ACCESSION B1736450  
 VERSION B1736450.1 GI:15713463  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgrahs-remail.nih.gov  
 Tissue Procurement: The Cepho Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM11932 row: 3 column: 21  
 High quality sequence stop: 709.  
 Location/Qualifiers  
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 Site\_2: SalI; Cloned unidirectionally; oligo-dt primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."  
 BASE COUNT 178 a 185 c 162 g 186 t  
 ORIGIN  
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 Best Local Similarity 89.0%; Pred. No. 4e-75;  
 Matches 532; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
 OY 2736 TACACAGACGAGGACTTTTGTGATCGAGGAGCTGTGATGAACAATTGCTA 2795  
 Db 114 TCCCTACAGACTGAGATTTTGTGAGTGAAGGAGCTGTCATGAACAAGTTGTTA 173  
 OY 2796 ACAATGGGCTCTTAAAGAATTACCTTATGACTACCAAGCATGCTGAGCCCAAC 2855  
 Db 174 ACAATGGGCTCTTAAAGAATTACCTTATGACTACCAAGCATGCTGAGCCCAAC 2855  
 OY 2856 AAGGAAGCAGGATGGGCCCATGCTCTGATGCTTAAAGCTTCTCTGTGA 2915  
 Db 234 AAGGAGACAGTGAAGAGTGGCTGCTGAGCCCTTAAGCCCTTCTCTGTGA 293  
 OY 2916 GTAATGATGATCAGCAAGCTTGTCTGCTGCTGAGATTTAACTCTGCAAGTTGG 2975  
 Db 294 GCCAAGTGATTAATGACGGAACCTGTCTTCTGCTGAGATTTAACTCTGCAAGTTGG 353

OY 2976 TGGCAGCTCCGATATGACAGCTTAAGCCCAAGAAATTGAACAGACCTTGGACCTTGTAT 3035  
 Db 354 TGGCAGCTCCGATATGACAGCTTAAGCCCAAGAAATTGAACAGACCTTGGAT 413  
 OY 3036 ACTGAATATCCAGATTCGTCTGAGGCGACCATCAAGAGAGTACAGGGAATATTTCT 3095  
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 OY 3096 TGTGAAGACTGCTCCAAAGTCTTTGTATCCAGCAAAATCCCAAGCAGCAACCTTTCATG 3155  
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 OY 3156 GTGTGTGTGAGCAGCAGTGTGCTGTGTAATCTGTGCCCCCATCACCATGACCATTT 3215  
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 OY 3216 GAATCAGGTATTAATGAATCCTTAAGTGAAGTGAAGGCGCAAGATCAGAAAG 3275  
 Db 594 GAATCAGGTATTAATGAATCCTTAAGTGAAGTGAAGGCGCAAGATCAGAAAG 653  
 OY 3276 CGCCAGAAATCTTGTCAATGCTTCATCTGAGGAGATGCAAGGAGTGTGGGCTG 3333  
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 BF465072 589 bp mRNA linear EST 04-DEC-2000  
 LOCUS BF465072  
 DEFINITION UI-M-CG0p-bqg-d-09-0-UI-s1 NIH\_BMAP\_Ret4\_S2 Mus musculus cDNA clone  
 UI-M-CG0p-bqg-d-09-0-UI 3', mRNA sequence.  
 ACCESSION BF465072  
 VERSION BF465072.1 GI:11534255  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgrahs-remail.nih.gov  
 Tissue Procurement: The Cepho Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM11932 row: 3 column: 21  
 High quality sequence stop: 709.  
 Location/Qualifiers  
 1. 589  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone IMAGE:5366516  
 /clone\_lib="NIH\_MGC\_94"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: eye; Vector: PCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dt primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."  
 BASE COUNT 178 a 185 c 162 g 186 t  
 ORIGIN  
 Query Match 13.1%; Score 492.4; DB 13; Length 711;  
 Best Local Similarity 89.0%; Pred. No. 4e-75;  
 Matches 532; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
 OY 2736 TACACAGACGAGGACTTTTGTGATCGAGGAGCTGTGATGAACAATTGCTA 2795  
 Db 114 TCCCTACAGACTGAGATTTTGTGAGTGAAGGAGCTGTCATGAACAAGTTGTTA 173  
 OY 2796 ACAATGGGCTCTTAAAGAATTACCTTATGACTACCAAGCATGCTGAGCCCAAC 2855  
 Db 174 ACAATGGGCTCTTAAAGAATTACCTTATGACTACCAAGCATGCTGAGCCCAAC 2855  
 OY 2856 AAGGAAGCAGGATGGGCCCATGCTCTGATGCTTAAAGCTTCTCTGTGA 2915  
 Db 234 AAGGAGACAGTGAAGAGTGGCTGCTGAGCCCTTAAGCCCTTCTCTGTGA 293  
 OY 2916 GTAATGATGATCAGCAAGCTTGTCTGCTGCTGAGATTTAACTCTGCAAGTTGG 2975  
 Db 294 GCCAAGTGATTAATGACGGAACCTGTCTTCTGCTGAGATTTAACTCTGCAAGTTGG 353



NIH-BMAP-Ret4\_S2 library is a subtracted library,  
ultimately derived from mouse retina tissue libraries at  
various stages of development. For a detailed description  
of the library from which this clone was derived, please  
visit our web site at [brainest.eng.uiowa.edu](http://brainest.eng.uiowa.edu). The tissue  
for this library was contributed by Dr. Xin-Yuan Fu, Yale  
University School of Medicine  
TAG-LIB-NIH-BMAP-Ret4\_S2  
TAG-TISSUE-adult-retina  
TAG-SEQ-GTCAGCGCGCAC"

BASE COUNT 156 a 134 c 147 g 152 t  
ORIGIN

Query Match 12.7%: Score 479.4; DB 12; Length 589;  
Best Local Similarity 89.4%: Pred. No. 7.4e-73;  
Matches 516; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 2754 TTTTGTGAGAGTGGAGAGCTGTGATGAACAATGCTAACATGGCTCTTTAA 2813  
DB 13 TTTTGTGAGAGTGGAGAGCTGTGATGAACAATGCTAACATGGCTCTTTAA 72  
QY 2814 AGAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCAAAGAAAGCAGCATGCC 2873  
DB 73 AGAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCAAAGAAAGCAGCATGCC 132  
QY 2874 GCCCATGGCTCTGTGATCTTATTAATGCTCTGCGATTAATGATCATGACA 2933  
DB 133 GCCCATGGCTCTGTGATCTTATTAATGCTCTGCGATTAATGATCATGACA 192  
QY 2934 GAATTTGCTTGTCTGTGTGGAATTTAATCTGTGAGTGTGAGTGTGAGTGTGAG 2993  
DB 193 GAATTTGCTTGTCTGTGTGGAATTTAATCTGTGAGTGTGAGTGTGAGTGTGAG 252  
QY 2994 GCTAAGGCCGGAATTAATGAGACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3053  
DB 253 GCTAAGGCCGGAATTAATGAGACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 312  
QY 3054 GCTCTGAGGCGACCATCAAGAGACTAAGGAATATTGCTGTGAAGACTGCTCAAG 3113  
DB 313 GCTCTGAGGCGACCATCAAGAGACTAAGGAATATTGCTGTGAAGACTGCTCAAG 372  
QY 3114 TCCCTTGTCAATCCAGCAATCCAGCAGCAACCTGTTCATGTGTGTGAGCAGCAGC 3173  
DB 373 TCCCTTGTCAATCCAGCAATCCAGCAGCAACCTGTTCATGTGTGTGAGCAGCAGC 432  
QY 3174 TGCCTGTGAATCTGTGGCCCATCAGCATGGCAGCCATGTGAATCAGTATATGAA 3233  
DB 433 TGCCTGTGAATCTGTGGCCCATCAGCATGGCAGCCATGTGAATCAGTATATGAA 492  
QY 3234 TCCCTTAAGTGTGAGCTTAAGAGCCAGAGATCAGAGAGCCAGCAATCTGTGCAT 3293  
DB 493 TCCCTTAAGTGTGAGCTTAAGAGCCAGAGATCAGAGAGCCAGCAATCTGTGCAT 552  
QY 3294 GCGTTCATCTCTGAGAGAAATGCAAGGAGTGTGGG 3330  
DB 553 GCGTTCATCTCTGAGAGAAATGCAAGGAGTGTGGG 589

Search completed: April 28, 2003, 01:17:00  
Job time : 4644 secs

GenCore version 5.1.5  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2003, 16:41:31 ; Search time 774 Seconds  
(without alignments)  
10969.036 Million cell updates/sec

Title: US-09-787-657-3

Perfect score: 3770

Sequence: 1 tactatagggcgccgcaa.....aaaaaaaaaaaaaaaaaa 3770

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3769.6	100.0	3770	21	AAA09253
2	3769.6	100.0	3770	22	AAAS01414
3	3769.6	100.0	3770	22	AAAF57551
4	3604.8	95.6	3690	24	AAAD26399
5	3399.2	90.2	3598	21	AAAO9261
6	3166.6	84.0	3213	22	AAAS01409
7	3166.6	84.0	3213	22	AAAF57546
8	3113.6	82.6	3114	22	AAAS01408
9	3113.6	82.6	3114	22	AAAF57545

10	3056.6	81.1	3057	22	AAAS01407	Human secreted sol
11	3056.6	81.1	3057	22	AAAF57544	Human calcium chan
12	1908.2	50.6	2008	21	AAA09260	Human alpha-2-delt
13	1545	41.0	1774	21	AAE51626	Human membrane cha
14	1268.2	33.6	3345	24	AAAS17582	DNA encoding novel
15	1268.2	33.6	5073	21	AAA09254	Human alpha-2-delt
16	1265.6	33.6	3228	24	AAAS17581	DNA encoding novel
17	1211.6	32.1	3209	22	AAAS01432	Human secreted sol
18	1211.6	32.1	3209	22	AAAF57569	Human calcium chan
19	1197.4	31.8	3339	22	AAAS01433	Human secreted sol
20	1197.4	31.8	3339	22	AAAF57570	Human calcium chan
21	1155.8	30.7	5713	21	AAA09278	Human alpha-2-delt
22	1139.6	30.2	3201	22	AAAS01431	Human secreted sol
23	1139.6	30.2	3201	22	AAAF57568	Human calcium chan
24	933	24.7	4125	24	AAAD22004	Human Transporets
25	837.6	22.2	1036	21	AAA09268	Probe for northern
26	755.6	20.0	859	22	AAI94285	Human neuroblastom
27	660.2	17.5	881	22	AAI94363	Human alpha-2-delt
28	596	15.8	1452	21	AAA09279	Human protein enco
29	502.2	13.3	1194	22	AAH99517	DNA encoding novel
30	423	11.2	783	23	AAH74094	Partial rat alpha-
31	390.4	10.4	516	21	AAA09290	Human secreted sol
32	293.4	7.8	1050	22	AAAS01412	Human calcium chan
33	293.4	7.8	1050	22	AAAF57549	Human secreted sol
34	248.6	6.6	969	22	AAAS01411	Human secreted sol
35	248.6	6.6	969	22	AAAF57548	Human calcium chan
36	235.6	6.2	912	22	AAAF57547	Human secreted sol
37	235.6	6.2	912	22	AAAF57547	Human calcium chan
38	232.8	6.2	274	21	AAA09292	Partial rat alpha-
39	214	5.7	3186	22	AAAS01404	Human secreted sol
40	214	5.7	3186	22	AAAF57541	Human calcium chan
41	214	5.7	3248	22	AAAS01405	Human secreted sol
42	214	5.7	3248	22	AAAF57542	Human calcium chan
43	214	5.7	3327	22	AAAS01406	Human secreted sol
44	214	5.7	3327	22	AAAF57543	Human calcium chan
45	214	5.7	5482	21	AAA09255	Human alpha-2-delt

## ALIGNMENTS

RESULT 1	AAA09253	standard: cDNA; 3770 BP.
ID	AAA09253	
AC	AAA09253;	
XX		
DT	10-AUG-2000	(first entry)
DE	Human alpha-2-delta-C gene.	
XX		
KW	alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cytostatic;	
KW	anticonvulsant; antimitigane; antiparkinsonian; antidepressant; ss.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	144..3401
XX		/*tag= a
XX	WO200020450-A2.	
XX		
PD	13-APR-2000.	
XX		
PF	07-OCT-1999;	99WO-US23519.
XX		
PR	07-OCT-1998;	98US-0103322.
PR	30-OCT-1998;	98US-0106473.
PR	29-DEC-1998;	98US-0114088.
XX		
PA	(WARN ) WARNER LAMBERT CO.	
XX		
PI	Johns MA, Moldover B, Offord JD.	

DR WP1: 2000-303744/26.  
DR P-PSDB: AAY92320.  
XX  
XX  
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D  
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,  
PT anxiety, multiple sclerosis or cancer  
XX  
XX  
PS Claim 1; Page 63-64; 88pp: English.  
XX  
CC The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.  
CC The gene has been mapped to chromosome 3p21.1. This gene and the related  
CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells  
CC from abnormal calcium flux by introducing expression vectors containing  
CC the respective gene into mammalian cells. The antisense genes are also  
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein  
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.  
CC Therefore, alpha-delta-2 proteins may also be targeted to treat  
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic  
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),  
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or  
XX addiction syndromes, mood, depression or cancer.  
XX  
XX Sequence 3770 BP; 1049 A; 871 C; 941 G; 908 T; 1 other;

Query Match	100.0%	Score 3769.6	DB 21	Length 3770
Best Local Similarity	100.0%	Pred. NO. 0		
Matches 3770	0	Mismatches	0	Gaps 0

OY	1	TACTATAGGGGGGGGGGCAATTTCCGACAGAGCGGGGGAGCCGAGACAGGCAACCCCGC	60
Db	1	TACTATAGGGGGGGGGGCAATTTCCGACAGAGCGGGGGAGCCGAGACAGGCAACCCCGC	60
OY	61	GGCGTCGGCCACCGCCCGCTCCGCGACACTCCCGCGCGCGCTCTCGTCGGCGCGGAGC	120
Db	61	GGCGTCGGCCACCGCGCGCTCCGCGACACTCCCGCGCGCGCTCTCGTCGGCGCGGAGC	120
OY	121	GGGCGCGCTCGAGGGAGGCCACATGGCCGGGGCGGCTGGCGCGCGCGCGCTCCGGG	180
Db	121	GGGCGCGCTCGAGGGAGGCCACATGGCGGGGGCGGCGCTGGCGCGCGCGCGCTCCGGG	180
OY	181	GGGCGCTCGGCGCTTCTCGCTCCGCGGCTTCTTCAAGCGCGCGCTGGGGAGCTGGTGGCT	240
Db	181	GGGCGCTCGGCGCTTCTCGCTCCGCGGCTTCTTCAAGCGCGCGCTGGGGAGCTGGTGGCT	240
OY	241	CGGAGCAGCAGATACCGCTCTCGGTGGAACTCTGGGCGCTCGGCTTTTGTGGGGAGA	300
Db	241	CGGAGCAGCAGATACCGCTCTCGGTGGAACTCTGGGCGCTCGGCTTTTGTGGGGAGA	300
OY	301	TAAATTCATTGGCTGCTTACGTACTCCGGTTCCCGACTTTCGCAAAAGAAATACAAAGAGT	360
Db	301	TAAATTCATTGGCTGCTTACGTACTCCGGTTCCCGACTTTCGCAAAAGAAATACAAAGAGT	360
OY	361	ATGAGAAAGACGTTGCCATGAAAGAAATTTATGGCTCCCAACTGGTAAAGAACTGGCAA	420
Db	361	ATGAGAAAGACGTTGCCATGAAAGAAATTTATGGCTCCCAACTGGTAAAGAACTGGCAA	420
OY	421	AGAACATCGAAGAAATGTTTTCACAGAAGTCTGAGGCGCTGACGCGCTGTGGAGGCTG	480
Db	421	AGAACATCGAAGAAATGTTTTCACAGAAGTCTGAGGCGCTGACGCGCTGTGGAGGCTG	480
OY	481	CAGAAAGACGACACTTGAACATGAATTTGATCAGAGCTTACAGTAAATGATCTTCAAG	540
Db	481	CAGAAAGACGACACTTGAACATGAATTTGATCAGAGCTTACAGTAAATGATCTTCAAG	540
OY	541	CTGTGCTGATTAATGAAAGGAGACAAGACGCGGAATTTTGGAGCTGGGAAAGAAATTTA	600
Db	541	CTGTGCTGATTAATGAAAGGAGACAAGACGCGGAATTTTGGAGCTGGGAAAGAAATTTA	600
OY	602	TCTTAGCCCCCAATGACATTTTAAATTAATTTGGCTGTGAACATCACTGTAAGTAGAGCTCC	660
Db	601	TCTTAGCCCCCAATGACATTTTAAATTAATTTGGCTGTGAACATCACTGTAAGTAGAGCTCC	660

Qy	661	AAGTACCAACGACATGTCAACAAAGACCCTGGCAATGTCAATGGGTTATATGGCTG	720
Db	661	AAGTACCAACGACATGTCAACAAAGACCCTGGCAATGTCAATGGGTTATATGGCTG	720
Qy	721	AATCTCTAAACAAAGTTTTGTAGATTAATCTTGTGACCGGTACCCTATCTCATATGGCAGT	780
Db	721	AATCTCTAAACAAAGTTTTGTAGATTAATCTTGTGACCGGTACCCTATCTCATATGGCAGT	780
Qy	781	ACTTTGGAAAGTGCAAAAGGCTTTTTAGGCAGTATCCGGGATTTAAATGGAACCAAGATG	840
Db	781	ACTTTGGAAAGTGCAAAAGGCTTTTTAGGCAGTATCCGGGATTTAAATGGAACCAAGATG	840
Qy	841	AGAAATGAGTCATTTGGCTTCGACCTCGAGGAACCCGAAATTTGTTACATCCAGCAGCAACTT	900
Db	841	AGAAATGAGTCATTTGGCTTCGACCTCGAGGAACCCGAAATTTGTTACATCCAGCAGCAACTT	900
Qy	901	CTCCGAAAGACGTGGCTCATTTAGTTAGATGGACGTCAGGAGCATGAAGAGACTCCGCTGTGA	960
Db	901	CTCCGAAAGACGTGGCTCATTTAGTTAGATGGACGTCAGGAGCATGAAGAGACTCCGCTGTGA	960
Qy	961	CTATCCCGAAGCAAAACAGTCTTCATCCATTTTGGATACACTTTGGGGATGATGACTTCTTGA	1020
Db	961	CTATCCCGAAGCAAAACAGTCTTCATCCATTTTGGATACACTTTGGGGATGATGACTTCTTGA	1020
Qy	1021	ACATTAATGCTTATATAGAGGAGCTTCACATTTGTGGAACCTTGGCTGTAAATGGAACCTTTGG	1080
Db	1021	ACATTAATGCTTATATAGAGGAGCTTCACATTTGTGGAACCTTGGCTGTAAATGGAACCTTTGG	1080
Qy	1081	TGCAAGCCGACAGGACAAACAAAGACACTTCAGGAGACATCTGGACAAACCTTTGGCA	1140
Db	1081	TGCAAGCCGACAGGACAAACAAAGACACTTCAGGAGACATCTGGACAAACCTTTGGCA	1140
Qy	1141	AAGGAATTGGAATGTTGGATTAAGCTCTGAATGAGGCCCTTCAACATTTCTGATGATTTCA	1200
Db	1141	AAGGAATTGGAATGTTGGATTAAGCTCTGAATGAGGCCCTTCAACATTTCTGATGATTTCA	1200
Qy	1201	ACCACACGGGACAAAGAAAGTATCTGCACTACAGCCATCATGCTCATTACTGATGGGGCGG	1260
Db	1201	ACCACACGGGACAAAGAAAGTATCTGCACTACAGCCATCATGCTCATTACTGATGGGGCGG	1260
Qy	1261	TGGACACCTCATTCATCAATCTTTGCCAAATTAACAATTTGGCCAGATTCGAAGGTTCCGATCT	1320
Db	1261	TGGACACCTCATTCATCAATCTTTGCCAAATTAACAATTTGGCCAGATTCGAAGGTTCCGATCT	1320
Qy	1321	TCACATACCTCATTTGGACAGAGAGCTCGCTTGGCAGCAATCTAAAGTGGATGGCCCTGG	1380
Db	1321	TCACATACCTCATTTGGACAGAGAGCTCGCTTGGCAGCAATCTAAAGTGGATGGCCCTGG	1380
Qy	1381	CCAAACAAAGATTTTTTACCAGATCTCCACACTTGGCTGATGTGCGAGGAATGTCTATGG	1440
Db	1381	CCAAACAAAGATTTTTTACCAGATCTCCACACTTGGCTGATGTGCGAGGAATGTCTATGG	1440
Qy	1441	AATACCTTCACAGTGTTAGCGCGGCCAAACATCAATCCACAGAGAGCATGATTTGGTGGTGA	1500
Db	1441	AATACCTTCACAGTGTTAGCGCGGCCAAACATCAATCCACAGAGAGCATGATTTGGTGGTGA	1500
Qy	1501	CCGAAAGCTTACATTGACAGCACTCTGACTGATGATGAGGGCCCGCTCGATGACACACCTG	1560
Db	1501	CCGAAAGCTTACATTGACAGCACTCTGACTGATGATGAGGGCCCGCTCGATGACACACCTG	1560
Qy	1561	TAGCAGTCCCTGCTGTTTATGTAAGCAGAAACAGATCGAAGGGCATTTCTTGGGAG	1620
Db	1561	TAGCAGTCCCTGCTGTTTATGTAAGCAGAAACAGATCGAAGGGCATTTCTTGGGAG	1620
Qy	1621	TGGTTGGCAGAGATGCCAGTAAGAAACCTTGTGAAGACATCCCCCAATTAACAAGTTAG	1680
Db	1621	TGGTTGGCAGAGATGCCAGTAAGAAACCTTGTGAAGACATCCCCCAATTAACAAGTTAG	1680
Qy	1681	GGATTTCACAGGTTATGCTTTGGCAATCAACAATTAATGGTATATCTCGAGCGCATCCGGAC	1740
Db	1681	GGATTTCACAGGTTATGCTTTGGCAATCAACAATTAATGGTATATCTCGAGCGCATCCGGAC	1740
Qy	1741	TCAGAGCTGCTGTACGAAGAAAGAAACCGAAGAAACCTAACTATATGATGACTTGGACC	1800

Db	1741	TCAGGCTGCTGTCAGAAAGAAAGAAAAAGCAAGGAACCTA	CTACTACTAGTAGCTTGACC	1800
Qy	1801	TCCTCTAGAGGTGGAGTGGGAAGACCGAGATGACGTGTTGAGA	AAATGCTTAAGGTGAATCGAA	1860
Db	1801	TCCTCTAGAGGTGGAGTGGGAAGACCGAGATGACGTGTTGAGA	AAATGCTTAAGGTGAATCGAA	1860
Qy	1861	AGACGGGGGAAGTTTCCATCCTGAGAGTGAAGAAGACAGT	GGACACCAAGGGAAACGGGTTTTGG	1920
Db	1861	AGACGGGGGAAGTTTCCATCCTGAGAGTGAAGAAGACAGT	GGACACCAAGGGAAACGGGTTTTGG	1920
Qy	1921	TCATGACCAAAATGACCTACTATTTATACAGACATCAAGG	TACTCCTTTAGTTAGTGTGG	1980
Db	1921	TCATGACCAAAATGACCTACTATTTATACAGACATCAAGG	TACTCCTTTAGTTAGTGTGG	1980
Qy	1981	CGCTTTCCAGAGGTGCATGGGAAATATTTCTCCGAGGGAA	TGTAAACCAAGGAAGGCC	2040
Db	1981	CGCTTTCCAGAGGTGCATGGGAAATATTTCTCCGAGGGAA	TGTAAACCAAGGAAGGCC	2040
Qy	2041	TGCTATACCTTAGAACAATCCCGATGTGTCTTGGCAGAT	GAATGTGCTTCTGCAACACTG	2100
Db	2041	TGCTATACCTTAGAACAATCCCGATGTGTCTTGGCAGAT	GAATGTGCTTCTGCAACACTG	2100
Qy	2101	ACCTACACCTTGAGCAACCGCATCTGCTCTGATAGAGG	GAATTAACCTTACTACTAAAG	2160
Db	2101	ACCTACACCTTGAGCAACCGCATCTGCTCTGATAGAGG	GAATTAACCTTACTACTAAAG	2160
Qy	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGTGAT	CCAAAGAGTCTTTTTGACCGG	2220
Db	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGTGAT	CCAAAGAGTCTTTTTGACCGG	2220
Qy	2221	TGCTGAGTGCCTCCCATTTGAAGCTATTTGACACAGCCT	GCCTTCACAAATCTGAAATTT	2280
Db	2221	TGCTGAGTGCCTCCCATTTGAAGCTATTTGACACAGCCT	GCCTTCACAAATCTGAAATTT	2280
Qy	2281	CTGACACAGGGCGTGGAGGTGTGCTTCTCTGGCACTG	GCACAGGGGCTCTCTCCAGATCAAC	2340
Db	2281	CTGACACAGGGCGTGGAGGTGTGCTTCTCTGGCACTG	GCACAGGGGCTCTCTCCAGATCAAC	2340
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Db	2341	TGTTGTTCGGGGCTGAGCAGCTCACCAATCAGAGATCTT	CTGAAAGCTGGCGACAAAGAGA	2400
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Db	2401	ACATTTTAAACGACGACCAATTTCCCTCTCTGTGAC	CGAAGAGCGGCTGAGCAGATTCCAG	2460
Qy	2461	GGAGCTGCTCTACTTCGATGCCATTTAGCACTGGAC	AGCAATTAAGCAATGTGTGTA	2520
Db	2461	GGAGCTGCTCTACTTCGATGCCATTTAGCACTGGAC	AGCAATTAAGCAATGTGTGTA	2520
Qy	2521	CAGCAAGTACATCCATCCAGCTCCCTGATGAAGGAAAT	CTCTTGATGGCAGCTGTAG	2580
Db	2521	CAGCAAGTACATCCATCCAGCTCCCTGATGAAGGAAAT	CTCTTGATGGCAGCTGTAG	2580
Qy	2581	GCATTCAGATGAAACTTGAATTTTCCAAAGGAAGTTT	CGACTGCACAGACAGTGTG	2640
Db	2581	GCATTCAGATGAAACTTGAATTTTCCAAAGGAAGTTT	CGACTGCACAGACAGTGTG	2640
Qy	2641	CTTCCCTGGATGGCAAAATCTCCATCAGCTGTGATAT	AGACTGTGAATTTGTACTCTCA	2700
Db	2641	CTTCCCTGGATGGCAAAATCTCCATCAGCTGTGATAT	AGACTGTGAATTTGTACTCTCA	2700
Qy	2701	TAGACAATTAATGATTTTATTTTGGTGTGGAAGACT	TAACACAGACATGGAGACTTTTTTG	2760
Db	2701	TAGACAATTAATGATTTTATTTTGGTGTGTGGAAGACT	TAACACAGACATGGAGACTTTTTTG	2760
Qy	2761	GTGAGATCGAGGAGCTGTGATGAACCAATTTGCTA	CAATGGGCTCTTTAAAGAATTA	2820
Db	2761	GTGAGATCGAGGAGCTGTGATGAACCAATTTGCTA	CAATGGGCTCTTTAAAGAATTA	2820
Qy	2821	CCCTTTATGACTTACCAAGCCATGTGTAGAGCC	ACAAGAAAGACAGATGCGCCCATG	2880
Db	2821	CCCTTTATGACTTACCAAGCCATGTGTAGAGCC	ACAAGAAAGACAGATGCGCCCATG	2880

Db	2821	CCCTTTATGACTACCAAGCCATGTGTAGACCAACAAGAAACACGATGGCGCCANTG	2881
QY	2881	GCCTCTCGATCCTTATATATGCTTCTCTCTGCTACGTAATAATGATCATGACAGACTTG	2940
Db	2881	GCCTCTCGATCCTTATATATGCTTCTCTCTGCTACGTAATAATGATCATGACAGACTTG	2940
QY	2941	TCTTGTTCCTGGTGGAAATTTAACTCTGACAGTTGGTGGCACTCCGATATGACAGCTAAAG	3000
Db	2941	TCTTGTTCCTGGTGGAAATTTAACTCTGACAGTTGGTGGCACTCCGATATGACAGCTAAAG	3000
QY	3001	CCCAAGAAATTAAGACAGACCCCTGGAGCCTTGATATCTGATATCCAGATTCGTCCTG	3060
Db	3001	CCCAAGAAATTAAGACAGACCCCTGGAGCCTTGATATCTGATATCCAGATTCGTCCTG	3060
QY	3061	AGCGCACCATCAAGAGACTACAGAGAAATATTCCTTGTGTGAAGACTGCTCCAAGCTTTTG	3120
Db	3061	AGCGCACCATCAAGAGACTACAGAGAAATATTCCTTGTGTGAAGACTGCTCCAAGCTTTTG	3120
QY	3121	TCATTCACAGCAATCCCAAGCAGCACTGTTCATGTGGTGGTGGACAGCACTGCTCT	3180
Db	3121	TCATTCACAGCAATCCCAAGCAGCACTGTTCATGTGGTGGTGGACAGCACTGCTCT	3180
QY	3181	GGGATCTGTGGCCCCCATATACCATGGCACCCTTAATAATCAGGTATATGAAATCCCTTA	3240
Db	3181	GGGATCTGTGGCCCCCATATACCATGGCACCCTTAATAATCAGGTATATGAAATCCCTTA	3240
QY	3241	AGTGTGAACGTCTTAAGAGCCACAGAAATCAGAGAGGCCACAGATCTTGTCACTGCTTC	3300
Db	3241	AGTGTGAACGTCTTAAGAGCCACAGAAATCAGAGAGGCCACAGATCTTGTCACTGCTTC	3300
QY	3301	ATTCGTAGAGAAATGCAAGGAGTGTGGGGGTGGCGCGAGTCTCCAAAGCCACAGACATCC	3360
Db	3301	ATTCGTAGAGAAATGCAAGGAGTGTGGGGGTGGCGCGAGTCTCCAAAGCCACAGACATCC	3360
QY	3361	TCTCTTCTGCTCCTCTCTCTCTTTTATGTCTCTTCCAAAGGTGACACTGATGATGTTCTC	3420
Db	3361	TCTCTTCTGCTCCTCTCTCTCTTTTATGTCTCTTCCAAAGGTGACACTGATGATGTTCTC	3420
QY	3421	TTACGACTGAGATGTTCTCTGTGCATGCTAAATTCATGATGATTAACGTGAACCAAAATAT	3480
Db	3421	TTACGACTGAGATGTTCTCTGTGCATGCTAAATTCATGATGATTAACGTGAACCAAAATAT	3480
QY	3481	GGTGCACATACGAGACATGATATATGTCACACCATCAGCATCTCATGATTTTAAAC	3540
Db	3481	GGTGCACATACGAGACATGATATATGTCACACCATCAGCATCTCATGATTTTAAAC	3540
QY	3541	TGTGCGGATATTAACCTCTTAAGAGATATGTTGACAAAAGTTATCTATCATCTTTTACT	3600
Db	3541	TGTGCGGATATTAACCTCTTAAGAGATATGTTGACAAAAGTTATCTATCATCTTTTACT	3600
QY	3601	TTGCGACGATGCAAAATGTAGATTTGGCACATGATATATACCCCTTCATCAGAAATGGGAC	3660
Db	3601	TTGCGACGATGCAAAATGTAGATTTGGCACATGATATATACCCCTTCATCAGAAATGGGAC	3660
QY	3661	CGCAAGTGTAGAGCAGTGTCTTCTGCTGTGAACCACTATTTGAACCAATTTAAACCTGTG	3720
Db	3661	CGCAAGTGTAGAGCAGTGTCTTCTGCTGTGAACCACTATTTGAACCAATTTAAACCTGTG	3720
QY	3721	TACTTTTAAATTAAGATATTTAAATTCATATAAAAAAAAAAAAAAAAAAAAAA 3770	
Db	3721	TACTTTTAAATTAAGATATTTAAATTCATATAAAAAAAAAAAAAAAAAAAAAA 3770	
RESULT 2			
AASeq1414			
ID	AASeq1414	standard; cDNA: 3770 BP.	
AASeq1414:			
XX	04-JUL-2001	(first entry)	
XX	Human secreted soluble alpha2delta calcium channel subunit #11 cDNA.		

KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
KM alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
KM filter binding assay; wheat germ lectin flashplate assay; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 144..3401  
FT /tag- a  
FT /product- "Alpha2delta calcium channel subunit #1"  
XX  
PN W0200119870-A2.  
XX  
PD 22-MAR-2001.  
XX  
PF 18-SEP-2000; 2000MO-EP09137.  
XX  
PR 16-SEP-1999; 990S-0397550.  
XX  
PA (WARN ) WARNER LAMBERT CO.  
XX  
PI Brown JP, Bertelli F;  
XX  
DR WPI: 2001-235262/24.  
DR P-PSDB; AAU01024.  
XX  
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
PT flashplate assays, Nickel flashplate assays, filter binding assays or  
PT wheat germ lectin flashplate assays -  
XX  
XX  
XX Claim 24; Page 93-94; 160pp; English.  
XX  
XX The present sequence encodes for human secreted calcium channel  
CC alpha2delta subunit #1 which is soluble and retains the functional  
CC characteristics of the full length or wild type alpha2delta subunit  
CC (AAU01025) from which it is derived. The invention relates to truncated  
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
CC which retain their affinity for radioactively labelled gabapentin. The  
CC alpha2delta subunit is 1 of the components of the heteromultimeric  
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
CC soluble forms of the human calcium channel alpha2delta subunits  
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
CC described. The secreted soluble alpha2delta subunit may be used in assays  
CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
CC filter binding or wheat germ lectin flashplate assays to detect or  
CC measure the binding or interaction of a ligand (e.g. gabapentin,  
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine,  
CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
CC alpha2delta subunit.  
XX  
XX  
SQ Sequence 3770 BP; 1049 A; 871 C; 941 G; 908 T; 1 other;  
Query Match 100.0%; Score 3769.6; DB 22; Length 3770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 GGGCCTGGGCGCTTCGCTGCCGCCGCTTCCTACGCCCGCGCTGGGAGCTGTGGCCT 240  
Qy 241 CGAGCAGCAGATACCGCTCTCCGTGTGAAGCTCTGGGCTCGGCTTTGGTGGGAGA 300  
Db 241 CGGAGCAGCAGATACCGCTCTCCGTGTGAAGCTCTGGGCTCGGCTTTGGTGGGAGA 300  
Qy 301 TAAATCCATTGCTGTGAAGTACCTCGGTTCCCGCTTCTGCAAAATAAATACAAAGT 360  
Db 301 TAAATCCATTGCTGTGAAGTACCTCGGTTCCCGCTTCTGCAAAATAAATACAAAGT 360  
Qy 361 ATGAGAAAGACGTTCCATGAGAAAGAAATGATGGCTCCCACTGTGTAAAGCTGGCAA 420  
Db 361 ATGAGAAAGACGTTCCATGAGAAAGAAATGATGGCTCCCACTGTGTAAAGCTGGCAA 420  
Qy 421 AGAATATGAGAGATTTTTCACAGAAGCTGTAGGCCGTCAGGCGTCTGTGGAGCTG 480  
Db 421 AGAATATGAGAGATTTTTCACAGAAGCTGTAGGCCGTCAGGCGTCTGTGGAGCTG 480  
Qy 481 CAGAGAGACACCTGAAACATGAAATTTGATGACAGCTACAGTATGATCTCAATG 540  
Db 481 CAGAGAGACACCTGAAACATGAAATTTGATGACAGCTACAGTATGATCTCAATG 540  
Qy 541 CTGTGCTGATTAATGAAGGACAAAGACGGAATTTTGTGAGCTGGAAAGAAATTC 600  
Db 541 CTGTGCTGATTAATGAAGGACAAAGACGGAATTTTGTGAGCTGGAAAGAAATTC 600  
Qy 601 TCTTAGCCCCAAATGACCATTTTAATATTTTGCCTGTGAACATCACTAAGTACGCTC 660  
Db 601 TCTTAGCCCCAAATGACCATTTTAATATTTTGCCTGTGAACATCACTAAGTACGCTC 660  
Qy 661 AAGTACCAAGCAATGTACAAACAAAGACCTGCATTTGTCATTTGGGCTTATTTGGCTG 720  
Db 661 AAGTACCAAGCAATGTACAAACAAAGACCTGCATTTGTCATTTGGGCTTATTTGGCTG 720  
Qy 721 AATCTTAACAAAGTTTGTGATTAATTAATTTGACCTGTGACCTCATCTATATGACAGT 780  
Db 721 AATCTTAACAAAGTTTGTGATTAATTAATTTGACCTGTGACCTCATCTATATGACAGT 780  
Qy 781 ACTTTGGAAGTGAAGAGGCTTTTGAAGCATATCCGGGATTAATATGGAACCAAGATG 840  
Db 781 ACTTTGGAAGTGAAGAGGCTTTTGAAGCATATCCGGGATTAATATGGAACCAAGATG 840  
Qy 841 AGAATGAGATATGCTGCTGACGTGACGAGAACCGAAATGATCATCCAGCGCAACTT 900  
Db 841 AGAATGAGATATGCTGCTGACGTGACGAGAACCGAAATGATCATCCAGCGCAACTT 900  
Qy 901 CTCGGAAGACGTGTCTATTTAGTACGTCAAGTGGCAGCATGAAGAGACTCCGTCTGA 960  
Db 901 CTCGGAAGACGTGTCTATTTAGTACGTCAAGTGGCAGCATGAAGAGACTCCGTCTGA 960  
Qy 961 CTAATCCGAAGCAACAGTCTCATCTATTTGATGATACCTTGGGATGATGACTTCTTCA 1020  
Db 961 CTAATCCGAAGCAACAGTCTCATCTATTTGATGATACCTTGGGATGATGACTTCTTCA 1020  
Qy 1021 ACATATTTGCTATATATGAGAGCTTCACTATGTGGAACCTTGCCGATATGGAACCTTGG 1080  
Db 1021 ACATATTTGCTATATATGAGAGCTTCACTATGTGGAACCTTGCCGATATGGAACCTTGG 1080  
Qy 1081 TGCAGCCGACAGAGCAACAAACAAAGACACTTCAAGGAGCATGTGCAAACTTTTCGCA 1140  
Db 1081 TGCAGCCGACAGAGCAACAAACAAAGACACTTCAAGGAGCATGTGCAAACTTTTCGCA 1140  
Qy 1141 AAGGAATTTGGAATGTGTGATATAGCTCTGAATGAGGCTTCAACTTCTGAGTGAATTC 1200  
Db 1141 AAGGAATTTGGAATGTGTGATATAGCTCTGAATGAGGCTTCAACTTCTGAGTGAATTC 1200  
Qy 1201 ACCACAGGAGACAAAGAAATATCTGACAGTCCAGCCATATGCTCATTAATGATGGGCGG 1260  
Db 1201 ACCACAGGAGACAAAGAAATATCTGACAGTCCAGCCATATGCTCATTAATGATGGGCGG 1260  
Qy 1261 TGGACACCATATGATCAATCTTTGCAAAATACAAATTTGGCAGACATGAAGGTTCCATCT 1320  
Db 1261 TGGACACCATATGATCAATCTTTGCAAAATACAAATTTGGCAGACATGAAGGTTCCATCT 1320

Qy	1321	TCACATACCTATTGGACGAGAGCGCTGCCTTTGGAGACAATCTAAAGTGGATGGCTGTG	1380
Db	1321	TCACATACCTATTGGACGAGAGCGCTGCCTTTGGAGACAATCTAAAGTGGATGGCTGTG	1380
Qy	1381	CCACAAGGATTTTTTATCCCAAGATCTCCACCTTGGCTGATGTGCAGAGATGTCAATG	1440
Db	1381	CCACAAGGATTTTTTATCCCAAGATCTCCACCTTGGCTGATGTGCAGAGATGTCAATG	1440
Qy	1441	AATACCTTCAAGTCTTATAGCCGGCCAAAGTCATCGACACGAGACATGATGTGGTGTGGA	1500
Db	1441	AATACCTTCAAGTCTTATAGCCGGCCAAAGTCATCGACACGAGACATGATGTGGTGTGGA	1500
Qy	1501	CCGAAGCTTACATTGACAGCACTCTGACTGATGATCAGAGGCCCGCTCTGATGACCACTG	1560
Db	1501	CCGAAGCTTACATTGACAGCACTCTGACTGATGATCAGAGGCCCGCTCTGATGACCACTG	1560
Qy	1561	TAGCATGCGCTGTGTTTAGTAGAGACAACAAACAGATCGAAGGGCATCTCTTGAGGAG	1620
Db	1561	TAGCATGCGCTGTGTTTAGTAGAGACAACAAACAGATCGAAGGGCATCTCTTGAGGAG	1620
Qy	1621	TGGTTGGCACAGATGTCCCAAGTGAAGAATCTTGAAAGACATCCCAATACAAATTAG	1680
Db	1621	TGGTTGGCACAGATGTCCCAAGTGAAGAATCTTGAAAGACATCCCAATACAAATTAG	1680
Qy	1681	GGATTCACGCTTATGCTTTGGCAATCACAAAATATGGRATATCTGACATCCGGAAC	1740
Db	1681	GGATTCACGCTTATGCTTTGGCAATCACAAAATATGGRATATCTGACATCCGGAAC	1740
Qy	1741	TCAGGGCGCTGTACGAAGAAGAAAAAGCGAAGAAACCTAATCTATAGCGTTGACC	1800
Db	1741	TCAGGGCGCTGTACGAAGAAGAAAAAGCGAAGAAACCTAATCTATAGCGTTGACC	1800
Qy	1801	TCCTGAGGTGAGTGGGGAAGACCGAGATGACGTGTGGAATATGCTATGTGATCGAA	1860
Db	1801	TCCTGAGGTGAGTGGGGAAGACCGAGATGACGTGTGGAATATGCTATGTGATCGAA	1860
Qy	1861	AGACGGGGGAATTTTCCATGAGAGGTGAAGAGAACAAGTGAACAAAGGGAACGGGTTTGG	1920
Db	1861	AGACGGGGGAATTTTCCATGAGAGGTGAAGAGAACAAGTGAACAAAGGGAACGGGTTTGG	1920
Qy	1921	TGATGACAAATGACTCTATTATACGACATCAAGGCTACTCCTTTAGTTAGTGTGG	1980
Db	1921	TGATGACAAATGACTCTATTATACGACATCAAGGCTACTCCTTTAGTTAGTGTGG	1980
Qy	1981	CGCTTCCAGAGGTCTATGGGAATATTTTCCGAGGGGAATGTAACCATCGAAGAGGCC	2040
Db	1981	CGCTTCCAGAGGTCTATGGGAATATTTTCCGAGGGGAATGTAACCATCGAAGAGGCC	2040
Qy	2041	TGCATGACTTAGAACATCCCGATGTCTCTTGGCAGATGAATGGTCTTATGCAACACTG	2100
Db	2041	TGCATGACTTAGAACATCCCGATGTCTCTTGGCAGATGAATGGTCTTATGCAACACTG	2100
Qy	2101	ACCTACACCTTGAGACCGGCCCATCTGTCTCAGTTAGAAACGATTAAAGCTTAACCTAAAG	2160
Db	2101	ACCTACACCTTGAGACCGGCCCATCTGTCTCAGTTAGAAACGATTAAAGCTTAACCTAAAG	2160
Qy	2161	GCAAGAACCTCTGCTCCAGTGTGATTAAGAATGATCCAGAAGTCTCTTTTGACGCGG	2220
Db	2161	GCAAGAACCTCTGCTCCAGTGTGATTAAGAATGATCCAGAAGTCTCTTTTGACGCGG	2220
Qy	2221	TGGTGAATGCCCCCATTTGAAGCGATTTGGACAGAGCTGGCCCTCAACAAATCTGAAATTT	2280
Db	2221	TGGTGAATGCCCCCATTTGAAGCGATTTGGACAGAGCTGGCCCTCAACAAATCTGAAATTT	2280
Qy	2281	CTGACAAGGGGTGAGAGTTGCTTCTCTCGCACTCGCACGGGCTCTCCAGAAATCAACC	2340
Db	2281	CTGACAAGGGGTGAGAGTTGCTTCTCTCGCACTCGCACGGGCTCTCCAGAAATCAACC	2340
Qy	2341	TGTTTGTGGGGCTGAGAGCTCAACAATCGAGACTTCCTGAAGAGCTGTGACAAAGGAGA	2400
Db	2341	TGTTTGTGGGGCTGAGAGCTCAACAATCGAGACTTCCTGAAGAGCTGTGACAAAGGAGA	2400

QY	2401	ACATTTTAAACGACAGACCATTTCCCTCTCTGGTACCGAAGAGCCGCTGACACAGATTCCAG	2460
Db	2401	ACATTTTAAACGACAGACCATTTCCCTCTCTGGTACCGAAGAGCCGCTGACACAGATTCCAG	2460
QY	2461	GGAGCTTCGTACTCCGATCCCATTTCAAGCAGCTGAGCAGTCAATAAAGCAATGTGGTGA	2520
Db	2461	GGAGCTTCGTACTCCGATCCCATTTCAAGCAGCTGAGCAGTCAATAAAGCAATGTGGTGA	2520
QY	2521	CAGCAAGTACATCCATCCAGCTCCCTGGATATACGGAAATCTCTGGTGGGACGCTGTAG	2580
Db	2521	CAGCAAGTACATCCATCCAGCTCCCTGGATATACGGAAATCTCTGGTGGGACGCTGTAG	2580
QY	2581	GCATTTACAGATGAACCTTGAAATTTTCCAAAGGAAGTCTTGAGCTGCACAGACAGTGTG	2640
Db	2581	GCATTTACAGATGAACCTTGAAATTTTCCAAAGGAAGTCTTGAGCTGCACACAGAGTGTG	2640
QY	2641	CTTCCCGAGATGGCAATGCTCCATACGCTGTATGATGAGACTGGAATGTTAACCTCA	2700
Db	2641	CTTCCCGAGATGGCAATGCTCCATACGCTGTATGATGAGACTGGAATGTTAACCTCA	2700
QY	2701	TAGACAAATTAATGATTTATTTTGGTGTCTAAGACTACACAGACTGGAGACTTTTTTG	2760
Db	2701	TAGACAAATTAATGATTTATTTTGGTGTCTAAGACTACACAGACTGGAGACTTTTTTG	2760
QY	2761	GTCGATCGAGGAGAGCTGTGTGATGAACAAATTGCTTAACAATGGGCTCTTTAAAGAAATTA	2820
Db	2761	GTCGATCGAGGAGAGCTGTGTGATGAACAAATTGCTTAACAATGGGCTCTTTAAAGAAATTA	2820
QY	2821	CCCTTTATGACTACCAAGGCATGTGTAGAGCCACACAGAAAGACAGATGGCGCCCATG	2880
Db	2821	CCCTTTATGACTACCAAGGCATGTGTAGAGCCACACAGAAAGACAGATGGCGCCCATG	2880
QY	2881	GCCTTCCTGATTCCTTTAAATGCTTCCTCTCGACGTAAATGATTCATGACAGAACTTG	2940
Db	2881	GCCTTCCTGATTCCTTTAAATGCTTCCTCTCGACGTAAATGATTCATGACAGAACTTG	2940
QY	2941	TCTTTGTTCTGTGGATTTAAACCTTCAGTTGGTGGCAGCTCCATATGACAGCTAAAG	3000
Db	2941	TCTTTGTTCTGTGGATTTAAACCTTCAGTTGGTGGCAGCTCCATATGACAGCTAAAG	3000
QY	3001	CCGAGAAATTTGAAACAGACCCTGGAGCCTTGTGATCTGAATATCCAGACTTGTCTCTG	3060
Db	3001	CCGAGAAATTTGAAACAGACCCTGGAGCCTTGTGATCTGAATATCCAGACTTGTCTCTG	3060
QY	3061	AGGCAACCATCAAGAGAGACTACAGGAAATATGCTTGGAAAGCTGCTCCAAAGTCTTTG	3120
Db	3061	AGGCAACCATCAAGAGAGACTACAGGAAATATGCTTGGAAAGCTGCTCCAAAGTCTTTG	3120
QY	3121	TCATCCAGCAAAATCCCAAGCAGCAACTGTTCATGTTGGTGGAGCAGCAGCTGCTCT	3180
Db	3121	TCATCCAGCAAAATCCCAAGCAGCAACTGTTCATGTTGGTGGAGCAGCAGCTGCTCT	3180
QY	3181	GTGAATCTGTGGCCCCCATCAACCATGCGACCCATTGAATCAGTATTAAGAAATCCCTTA	3240
Db	3181	GTGAATCTGTGGCCCCCATCAACCATGCGACCCATTGAATCAGTATTAAGAAATCCCTTA	3240
QY	3241	AGTGTGAACGTTAATAGGCCACAGAAATCAAGAGGCCACAGAAATCTTGTCAATGAGCTTC	3300
Db	3241	AGTGTGAACGTTAATAGGCCACAGAAATCAAGAGGCCACAGAAATCTTGTCAATGAGCTTC	3300
QY	3301	ATCTGTAGAGAGATGCAAGGAGTGTGGGGGTGGCGGAGCTTCCAAAGCCACAGACAGTCC	3360
Db	3301	ATCTGTAGAGAGATGCAAGGAGTGTGGGGGTGGCGGAGCTTCCAAAGCCACAGACAGTCC	3360
QY	3361	TGCTTCCTCTCTCTCTGTTTGTATGCTCTTCTCAAGGTACACGTAGATGTTCTC	3420
Db	3361	TGCTTCCTCTCTCTCTGTTTGTATGCTCTTCTCAAGGTACACGTAGATGTTCTC	3420
QY	3421	TTACGACTGTGAGTTCCTCTGGCATGCTAAATCAATGATTAACGTGAACCAAAATAT	3480
Db	3421	TTACGACTGTGAGTTCCTCTGGCATGCTAAATCAATGATTAACGTGAACCAAAATAT	3480
QY	3481	GTGCGAACATACGAGACATGAATTAAGTCCACACATCAGATCTCATGTGATTTTAAAC	3540

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Db 3481 GGTGCACATGACGACATGATATAGTCAACCATGACATCATCATGATTTTAAAC 3540
Qy 3541 TTGCGGATATTAACCTTAAAGATATGTTGACAAAAAGTATATCATCTTTTACT 3600
Db 3541 TTGCGGATATTAACCTTAAAGATATGTTGACAAAAAGTATATCATCTTTTACT 3600
Qy 3601 TTGCGGATATTAACCTTAAAGATATGTTGACAAAAAGTATATCATCTTTTACT 3600
Db 3601 TTGCGGATATTAACCTTAAAGATATGTTGACAAAAAGTATATCATCTTTTACT 3600
Qy 3661 CGCAAGTGTAGGAGTGTCCCTTCTGTTGAAAACCTATTTTAAACCTGTG 3720
Db 3661 CGCAAGTGTAGGAGTGTCCCTTCTGTTGAAAACCTATTTTAAACCTGTG 3720
Qy 3721 TACTTTTAAATTAAGTATATTAATCATTAATAAAAAAAAAAAAAA 3770
Db 3721 TACTTTTAAATTAAGTATATTAATCATTAATAAAAAAAAAAAAAA 3770

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## RESULT 3

AAF57551 ID AAF57551 standard: DNA: 3770 BP.

AAF57551:  
11-JUN-2001 (first entry)

Human calcium channel alpha2delta subunit encoding DNA.

Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex; nervous system disorder; pain; epilepsy; anxiety; human; ds.

Homo sapiens.

Key Location/Qualifiers

CDS 144..3401

/\*tag= a

MO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000MO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN ) WARNER LAMBERT CO.

Bertelli F, Brown JP, Disanayake V, Suman-Chauhan N, Gee NS;

WPI; 2001-257902/26.

P-PSDB: AAB62248.

Competitive binding assay for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where the ligands identified are useful for treating disorders of the nervous system, including pain -

Disclosure: Page 92-93; 158pp; English.

The invention relates to a new method for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta subunit, preferably alpha2delta-1 subunit. The method comprises contacting a secreted soluble recombinant alpha2delta-1 subunit with a ligand of interest and a labelled compound which binds the subunit, followed by measuring the level of binding of the labelled compound to alpha2delta-1 subunit. The method is useful for screening ligands, preferably biologically active products that modulate a nervous system function, which bind a cerebral cortical voltage-dependent calcium channel alpha2delta-1 subunit. The ligands identified by the method are useful for treating disorders of the nervous system, including pain, epilepsy and anxiety. The present sequence represents a human calcium channel

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CC alpha2delta subunit encoding DNA.
XX
SQ Sequence 3770 BP; 1049 A; 871 C; 941 G; 908 T; 1 other:
Query Match 100.0%; Score 3769.6; DB 22; Length 3770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TACTATAGGGGGGGGGAATTCGGACAGAGCGCGGAGCGGACAGGACCCCGC 60
Db 1 TACTATAGGGGGGGGGAATTCGGACAGAGCGCGGAGCGGAGCGGACAGGACCCCGC 60
Qy 61 GCGCTCGCCCGCCCGCGCTCCGGAGCTCCCGGGCGGCTGTGCGCGCGGAGC 120
Db 61 GCGCTCGCCCGCCCGCGCTCCGGAGCTCCCGGGCGGCTGTGCGCGCGGAGC 120
Qy 121 GGGCGGCTGGAGGAGAGCCAGCATGGCCGGGCGGCGGCGGCGGCGGCGGCGG 180
Db 121 GGGCGGCTGGAGGAGAGCCAGCATGGCCGGGCGGCGGCGGCGGCGGCGGCGG 180
Qy 181 GGGCGGCTGGAGGAGAGCCAGCATGGCCGGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 GGGCGGCTGGAGGAGAGCCAGCATGGCCGGGCGGCGGCGGCGGCGGCGGCGG 240
Qy 241 CGGAGCAGAGATPACGCGCTCGGTGGTGAAGCTGGGGCGGCTTTGGTGGGAGA 300
Db 241 CGGAGCAGAGATPACGCGCTCGGTGGTGAAGCTGGGGCGGCTTTGGTGGGAGA 300
Qy 301 TAAATCCATTGCTGTCTAAGTACTCCGGTCCAGCTTCTGCAAAAGAAATACAAAGAT 360
Db 301 TAAATCCATTGCTGTCTAAGTACTCCGGTCCAGCTTCTGCAAAAGAAATACAAAGAT 360
Qy 361 ATGAGAAAGAGCTTGGCATGAAAGAAATTCATGAGCCCTCCACTGCTGAAGAGCTGGCAA 420
Db 361 ATGAGAAAGAGCTTGGCATGAAAGAAATTCATGAGCCCTCCACTGCTGAAGAGCTGGCAA 420
Qy 421 AGAATCATGAAAGATGTTTACACAGAAGCTGAGCGCGGCGGCTGTGGAGGCTG 480
Db 421 AGAATCATGAAAGATGTTTACACAGAAGCTGAGCGCGGCGGCTGTGGAGGCTG 480
Qy 481 CAGAGAGCAGACCTGAAACATGAATTTGATGACAGCTTACAGTATGATTAATCTTAATG 540
Db 481 CAGAGAGCAGACCTGAAACATGAATTTGATGACAGCTTACAGTATGATTAATCTTAATG 540
Qy 541 CTGTGCTGATTAATGAAGAGGACAAAGACGGGAAATTTTGGAGCTGGGAAGGAATTC 600
Db 541 CTGTGCTGATTAATGAAGAGGACAAAGACGGGAAATTTTGGAGCTGGGAAGGAATTC 600
Qy 601 TCTTACCCCAATGACATTTTAATTAATTTGCTGTGAACATCAGTCAAGGAGCTCC 660
Db 601 TCTTACCCCAATGACATTTTAATTAATTTGCTGTGAACATCAGTCAAGGAGCTCC 660
Qy 661 AAGTACCAAGCAATGATCAACAAAGACCTGCAATTTGTCATGGGCTTTATTTGCTCG 720
Db 661 AAGTACCAAGCAATGATCAACAAAGACCTGCAATTTGTCATGGGCTTTATTTGCTCG 720
Qy 721 AATCTTAACAAGTTTGTGATGATTAATCTTGAACCTGATCCATCTCTCATATGGCACT 780
Db 721 AATCTTAACAAGTTTGTGATGATTAATCTTGAACCTGATCCATCTCTCATATGGCACT 780
Qy 781 ACTTTGGAAGTCAAAAGGCTTTTATAGCAGTATCCGGGGGATTAAATGGGAACCAAGATG 840
Db 781 ACTTTGGAAGTCAAAAGGCTTTTATAGCAGTATCCGGGGGATTAAATGGGAACCAAGATG 840
Qy 841 AGAATGAGTCAATTCCTTGCAGCTGAGAGAACCAAAATGATACATCCAGAGCAACTT 900
Db 841 AGAATGAGTCAATTCCTTGCAGCTGAGAGAACCAAAATGATACATCCAGAGCAACTT 900
Qy 901 CTCGGAAGAGCTGTATTTAGTTGACGTGAGGCGAGCATGAAGAGCACTCGCTGCA 960
Db 901 CTCGGAAGAGCTGTATTTAGTTGACGTGAGGCGAGCATGAAGAGCACTCGCTGCA 960
Qy 961 CTAATGCGAAGCAACAGTCTCATCTTTTGGATACACTTGGGAGTATGACTTTTCA 1020

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Db 961 CTATCGGAAGCAAAAGTCTCATCCATTTTGGATACACTTGGGGATGATGACTTCTCA 1020
QY 1021 ACATTAATTCCTTTAAATGAGAGCTTACTATGGAACCTTGCCCTAATGGAACCTTGG 1080
Db 1021 ACATTAATTCCTTTAAATGAGAGCTTACTATGGAACCTTGCCCTAATGGAACCTTGG 1080
QY 1081 TGCAAGCCGACAGACAAACAAAGAGACCTTCAGAGAGCATCTGACAAACTTTTGCCA 1140
Db 1081 TGCAAGCCGACAGACAAACAAAGAGACCTTCAGAGAGCATCTGACAAACTTTTGCCA 1140
QY 1141 AAGGAATTTGGAATGTTGGATATAGCTTGATATAGAGCCCTTCAACATTTGAGTATTTCA 1200
Db 1141 AAGGAATTTGGAATGTTGGATATAGCTTGATATAGAGCCCTTCAACATTTGAGTATTTCA 1200
QY 1201 ACCACAGGAGCAAGGAAGATCTGACATGAGCCATGATCACTATACCTGATGAGGCGG 1260
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QY 1381 CCACAAAGGATTTTATCCAGATCTCCACCTTGAGCTGATGTCAGAGAGATGTCATG 1440
Db 1381 CCACAAAGGATTTTATCCAGATCTCCACCTTGAGCTGATGTCAGAGAGATGTCATG 1440
QY 1441 AATACCTTACGCTGTACCGGCCCAAGTCATCGACAGAGAGCATGATGTTGGTGG 1500
Db 1441 AATACCTTACGCTGTACCGGCCCAAGTCATCGACAGAGAGCATGATGTTGGTGG 1500
QY 1501 CCGAAGCTTACATTTGACAGACACTCTGATGATGATGAGGCCCCGTCCTGATGACCACTG 1560
Db 1501 CCGAAGCTTACATTTGACAGACACTCTGATGATGATGAGGCCCCGTCCTGATGACCACTG 1560
QY 1561 TAGCCATGCTGCTGTTTAAAGCAAGCAACCAAGATGCAAGGCACTTCTTCTGGAG 1620
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Db 1621 TGGTTGGCAGACATGTCACAGTGAAGAACTTCTGAGACCACTCCCAATATCAAGTTAG 1680
QY 1681 GGATTCACGGTTATGCCCTTTCGAATCACAATAATGRTATCTGACGCAATCCGGAAAC 1740
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Db 1741 TCAGGCTGCTGATGAGAAAGGAAAAAGCCGAAGAAACCTTAACATATGATACCTTTGACC 1800
QY 1801 TCTCTGAGAGTGGAGTGGGAAGACGAGATGACGTTGTGAGAAATGCTAT 3GGAATTCGAA 1860
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QY 1861 AGACGGGGAAGTTTTCATGAGAGTGAAGAGACAGTGGACAAAGGGAAGAGGCTTTTGG 1920
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QY 1981 CGCTTTCCAGAGCTATGGAAGAAATATTTCTCCGAGGGAATGTAACCAAT 3AAGAGGCC 2040
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Db 2461 GGAAGTTGCTTACTGATCCCAATGACGACTGGACAGCACTTCAATTAAGCAATGTTGTGA 2520
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Db 2521 CAGCAGTACATCCATCCAGCTCTGATGATGACGGAATCTCTGTGTGGGACGCTGTAG 2580
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Db 2701 TAGACAATAATGATTTATTTTGTGTCTGAGACTACACAGACTGAGACTTTTGG 2760
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    |||||||
DB 3181 GTGAAATCTGTGGCCCCCATCCATGCGACCCATTGGAATCAGGTATATGATCCCTTA 3240
OY 3241 AGTGTGACGCTTAAGAGCCGAGAAATCAGAAAGAGCCGCCAGAACTTGTTCATGGCTTCC 3300
    |||||||
DB 3241 AGTGTGAAACGCTTAAGAGCCGAGAAATCAGAAAGAGCCGCCAGAACTTGTTCATGGCTTCC 3300
OY 3301 ATCTGTGAGGAAATGCAAGGAGTGTGGGGTGGCCGAGTCTCCAAAGCCAGACAGTCC 3360
    |||||||
DB 3301 ATCTGTGAGGAAATGCAAGGAGTGTGGGGTGGCCGAGTCTCCAAAGCCAGACAGTCC 3360
OY 3361 TCCCTTGTGCTCCCTCTCTCTTTTGTATGCTTCTCAAGGTGACATCTGATGATGTTCTC 3420
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DB 3361 TCCCTTGTGCTCCCTCTCTCTTTTGTATGCTTCTCAAGGTGACATCTGATGATGTTCTC 3420
OY 3421 TTACTGACTGAGATGTTCTCTTGGCATGCTAAATCATGATGATGATGATGATGATGAT 3480
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DB 3421 TTACTGACTGAGATGTTCTCTTGGCATGCTAAATCATGATGATGATGATGATGATGAT 3480
OY 3481 GGTGCAACATACGAGACATGATATATCCACCATCAGCATCTCATCATGATGATTTAAAC 3540
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DB 3481 GGTGCAACATACGAGACATGATATATCCACCATCAGCATCTCATCATGATGATTTAAAC 3540
OY 3541 TGTGCGGATATTAACCTTAAGATATGTTGACAAAAGTTATCTATCATCTTTTACT 3600
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DB 3541 TGTGCGGATATTAACCTTAAGATATGTTGACAAAAGTTATCTATCATCTTTTACT 3600
OY 3601 TTGGCAGCATGCAAAATGATGATGATTTGGCAGATGATATCAACCTTCATCATGATTTTAAAC 3660
    |||||||
DB 3601 TTGGCAGCATGCAAAATGATGATGATTTGGCAGATGATATCAACCTTCATCATGATTTTAAAC 3660
OY 3661 CGGAAGGTGAGGAGGAGTGTCTCTGCTTGGAAACCTATGAAACCAATTTAAACCTGTG 3720
    |||||||
DB 3661 CGGAAGGTGAGGAGGAGTGTCTCTGCTTGGAAACCTATGAAACCAATTTAAACCTGTG 3720
OY 3721 TACTTTTAAATTAAGATATTTAAATCATTAATAAAAAAAAAAAAAAAAAAAAAA 3770
    |||||||
DB 3721 TACTTTTAAATTAAGATATTTAAATCATTAATAAAAAAAAAAAAAAAAAAAAAA 3770

RESULT 4
ID AAD26399 standard: cdna: 3690 BP.
XX
AC AAD26399:
XX
DT 22-APR-2002 (first entry)
DE
XX Human calcium channel family member, 21784 cDNA.
XX
KW Human: calcium channel family member; 21784; immunosuppressive; therapy;
KW neuroprotective; nootropic; cytoskeletal; autoimmune disease; arthritis;
KW multiple sclerosis; encephalomyelitis; myasthenia gravis; drug screening;
KW cognitive disorder; neurodegenerative; neuropsychiatric; cardiovascular;
KW neurological; sleep; memory; autonomic; cellular proliferative; immune;
KW liver; metabolic; diabetes mellitus; graft-versus-host disease; amnesia;
KW Alzheimer's disease; dementia; Huntington's disease; hypertension; pain;
KW schizophrenia; phobia; migraine; obesity; viral disease; tissue typing;
KW
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FT /*product= "Human 21784 protein"
FT /*note= "This region is specifically claimed as SEQ ID
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FT /*tag= b
FT mat_peptide 122..3301
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FT /*tag= c
FT /*product= "Mature 21784 protein"
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XX
XX PD 13-DEC-2001.
XX
XX PF 05-JUN-2001; 2001MO-US18398.
XX
XX PR 05-JUN-2000; 2000US-209257P.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Curtis RMJ;
XX
XX DR WPI: 2002-147674/19.
XX
XX DR P-PSDB: AAE16665.
XX
XX PT New 21784 polypeptides and polynucleotides, useful for e.g. treating or
XX preventing autoimmune diseases, such as arthritis, multiple sclerosis,
XX encephalomyelitis, myasthenia gravis, or graft-versus-host disease
XX
XX PS Claim 1; Page 104-106; 121pp; English.
XX
XX CC The invention relates to an isolated nucleic acid molecule encoding
XX calcium channel family member, designated as 21784. 21784 proteins are
XX useful as reagents or targets in the treatment and diagnosis of 21784-
XX mediated or -related disorders such as calcium channel-associated
XX disorders, to screen for drugs or compounds which modulate 21784 activity
XX and to treat disorders characterised by insufficient or excessive
XX production of 21784 protein. Calcium channel-associated disorders include
XX cognitive disorders and neurodegenerative disorders (Alzheimer's disease,
XX dementia, Huntington's disease), autonomic function disorders (sleep
XX disorders, hypertension), neuropsychiatric disorders (schizophrenia,
XX depression, Korsakoff's psychosis), learning or memory disorders (amnesia
XX age-related loss, attention deficit disorder, phobias) and bipolar
XX affective neurological disorder (migraine, obesity). 21784 molecules may
XX also be used as diagnostic targets and therapeutic agents for controlling
XX one or more cellular proliferative and/or differentiative disorders,
XX disorders associated with bone metabolism, immune disorders, liver
XX disorders, viral diseases, cardiovascular disorders, pain or metabolic
XX disorders. Nucleotide sequences are also used for chromosome mapping,
XX tissue typing, in predictive medicine, as markers of disorders or drug
XX activity, markers for precursors of disease states or for predisposition
XX of disease states, as well as for treating or preventing autoimmune
XX diseases, such as diabetes mellitus, arthritis, multiple sclerosis,
XX encephalomyelitis, myasthenia gravis, or graft-versus-host disease. The
XX present sequence is human 21784 cDNA.
XX
XX SQ Sequence 3690 BP; 1054 A; 831 C; 901 G; 900 T; 4 other:

Query Match 95.6%; Score 3604.8; DB 24; Length 3690;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3631; Conservative 3; Mismatches 0; Indels 18; Gaps 1;

OY 137 GCCACATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCT 196
    |||||||
DB 22 GCCACATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCT 81
OY 197 CGCTGCGCGCGCTTCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCT 256
    |||||||
DB 82 CGCTGCGCGCGCTTCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCT 141
OY 257 GCTCTCGTGTGAGACCTGTGGCGCTGCGCTTGTGTGGGAGATTAATCCATTGCTGC 316
    |||||||
DB 142 GCCTCTCGTGTGAGACCTGTGGCGCTGCGCTTGTGTGGGAGATTAATCCATTGCTGC 201
OY 317 TAAGTACTCGGTGCTCCAGCTTCTGCAAAAGAAATCAAGAGTATGAGAAAGACCTTGC 376
    |||||||
DB 202 TAAGTACTCGGTGCTCCAGCTTCTGCAAAAGAAATCAAGAGTATGAGAAAGACCTTGC 261
OY 377 CATGAGAAATTAAGTGTGCTCAACCTGTAAAGAGTGTGCAAAAGACATGGAAGAGAT 436
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Db 322 GTTTCACAAAGACTGTGAGGCCGTGAGGCCGTGTGTGGAGCTGCAGAAAGACACACCT 381
Oy 497 GAAACATGAATTTGATGACAGACTTACAGTATGAATACTTCAATCTGTGTATTAATGA 556
Db 382 GAAACATGAATTTGATGACAGACTTACAGTATGAATACTTCAATCTGTGTATTAATGA 441
Oy 557 AAGGCAAAAGAGCGGGAATTTTGGAGCTGGGAAAGAAAGATTCATCTTACCCTCAATGA 616
Db 442 AAGGCAAAAGAGCGGGAATTTTGGAGCTGGGAAAGAAAGATTCATCTTACCCTCAATGA 501
Oy 617 CCAATTTAATTAATTTGCTGTGAAACATCACTAAGTACGCTCAAGTACCAAGTACCAAGACAT 676
Db 502 CCAATTTAATTAATTTGCTGTGAAACATCACTAAGTACGCTCAAGTACCAAGTACCAAGACAT 561
Oy 677 GTTACAAAGAAAGCCCTGCAATTTGTCAATGAGGGTTTATGGTGTGAATCTTCTAAACAAAGT 736
Db 562 GTTACAAAGAAAGCCCTGCAATTTGTCAATGAGGGTTTATGGTGTGAATCTTCTAAACAAAGT 621
Oy 737 TTTTGTAGATTAATTTGACCGGTGACCCATCTCATATGGCACTACTTGTGAAGTGCATAA 796
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Oy 797 GGGCTTTTGTAGGACATATCCGGGGATTAATGGAACCAAGATGAGAAATGGAGTCAATTCG 856
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Oy 857 CTTCGACTGACAGAACCGGAAATGTGATCCAGGACGAACTTCTCCGAAAGACGTGTG 916
Db 742 CTTCGACTGACAGAACCGGAAATGTGATCCAGGACGAACTTCTCCGAAAGACGTGTG 801
Oy 917 CATTTAGTGTGACGTGAGGCGACATGGAAGGACCTCCCTGTGACATATGGCGAAGCAAC 976
Db 802 CATTTAGTGTGACGTGAGGCGACATGGAAGGACCTCCCTGTGACATATGGCGAAGCAAC 861
Oy 977 AGTCTCATCATTTTGGATGATACACTTGGGGATGATGACTCTTTCACATATATTGCTTATAA 1036
Db 862 AGTCTCATCATTTTGGATGATGATGACTTGGGGATGATGACTCTTTCACATATATTGCTTATAA 921
Oy 1037 TTAGGAGCTTCACTATGTGAAACCTTGGCTGAATGGAACCTTGGTGGCAAGCCGACAGAG 1096
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Db 982 AAACAAAGAGCACTTCAGGAGCATCTGACAAACCTTTCCGCCAAAGGAATTTGGAATTT 1041
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Db 1042 GGATATAGCTGGAATGAGGCGCTTCAACATTTGTAGTATTTCAACCAACAGGGACAAG 1101
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Db 1102 AAGTATTCGACGTCAAGCCATCATCTCATTAACCTGATGGGGGGGTGACACCTATGATAC 1161
Oy 1277 AATCTTTCGAAATATCAATTTGGCCAGATCGAAAGTTGGCATCTTTCACATACCTATTTGG 1336
Db 1162 AATCTTTCGAAATATCAATTTGGCCAGATCGAAAGTTGGCATCTTTCACATACCTATTTGG 1221
Oy 1337 AAGAGAGGCTGCTTTCGAGACAATCTAAAGTGAATGGCTGTGGCCACAAAGGAATTTT 1396
Db 1222 AAGAGAGGCTGCTTTCGAGACAATCTAAAGTGAATGGCTGTGGCCACAAAGGAATTTT 1281
Oy 1397 TACCAGATTCACACTTGGCTGATGTGCAGAGAGATGTCAATGAATACCTTTCACAGTGTCT 1456
Db 1282 TACCAGATTCACACTTGGCTGATGTGCAGAGAGATGTCAATGAATACCTTTCACAGTGTCT 1341
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Db 1342 TAGCCGCGCCAAAGTCAATCGACAGAGAGCATGATGGTGTGGACCGGAA3CTTACATTGA 1401

Oy 1517 CAGCACT-----CTGACTGATGATCAGGGCCCGCTCCGTGATGACCAC 1558
Db 1402 CAGCACTCTCCCTCAGGCACAAAAAGCTGACTGATGATCAGGGCCCGCTCCGTGATGACCAC 1461
Oy 1559 TGTAGCCATGCTGTGTGTGTAGTAAGCAGAAAGCAAGACAGATTCGAAAGGCAATTTCTTGGG 1618
Db 1462 TGTAGCCATGCTGTGTGTGTGTAGTAAGCAGAAAGCAAGACAGATTCGAAAGGCAATTTCTTGGG 1521
Oy 1619 AGTGTGTGACAGATGTCCAGTGAAGAACTTTCGAGACCATCCCAATATCAAGTT 1678
Db 1522 AGTGTGTGACAGATGTCCAGTGAAGAACTTTCGAGACCATCCCAATATCAAGTT 1581
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Oy 1739 ACTGAGGCTCTGTACGAAAGGAAAGAAAGCAAGGAAACCTAATATATATGATGAGCTTGA 1798
Db 1642 ACTGAGGCTCTGTACGAAAGGAAAGAAAGCAAGGAAACCTAATATATATGATGAGCTTGA 1701
Oy 1799 CTTCTCTGAGGTGAGTGGGAAAGACGAGATGACGTGTTGAGAAATGCTATGTTGATTCG 1858
Db 1702 CTTCTCTGAGGTGAGTGGGAAAGACGAGATGACGTGTTGAGAAATGCTATGTTGATTCG 1761
Oy 1859 AAGAGCGGGGAATTTTCCATGAGAGTGAAGAAAGACAGTGGACAAAGGCAACGGTTTT 1918
Db 1762 AAGAGCGGGGAATTTTCCATGAGAGTGAAGAAAGACAGTGGACAAAGGCAACGGTTTT 1821
Oy 1919 GGTGATGACAAATGACTATATATACAGATCAAGGGGATCTCTTTCAGTTAGGTGT 1978
Db 1822 GGTGATGACAAATGACTATATATACAGATCAAGGGGATCTCTTTCAGTTAGGTGT 1881
Oy 1979 GGGCTTTTCCAGAGTCAATGGAATATTTCTTCCAGGGAATGTAACCATGCAAGAAAG 2038
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Oy 2039 CTTGCAATGACTTGAACATCTCCGATGTGCTTGGAGATGAATGGTCTTACTGCAACAC 2098
Db 1942 CTTGCAATGACTTGAACATCTCCGATGTGCTTGGAGATGAATGGTCTTACTGCAACAC 2001
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Db 2182 TTCTGCAAGGGCGTGGAGGTTGCCCTCTCTGCGCACTGCGACAGGGGCTCTCCAGAAATCAA 2241
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Db 2242 CCTGTTTGTGGGGGCTGAGACAGCTCACCAGATCAGGACTCTGAAAGCTGGGAGCAAGGA 2301
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Db 2362 AAGGAGCTTTCGTCTACTGATCCCATTCAGACCTGAGACAGATTAAGAGAAATGTGCT 2421
Oy 2519 GACAGCAAGTACATCATCTCAGCTCCTGATGAAGAAAGAAATCTCTGTGTGGACAGCTGT 2578
Db 2422 GACAGCAAGTACATCATCTCAGCTCCTGATGAAGAAAGAAATCTCTGTGTGGACAGCTGT 2481
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Db	2482	AGGCATTCAGATGAAACCTTGAATTTTTC	CCAAAGCAAGTTC	CTGACATGCCACAGACAGT	254.1
OY	2639	TGCTTCCCTGGATGGCAAAATGCTCCATC	CAGCTGGATGATGATAGACATGGATTTGTTACCT		2698
Db	2542	TGCTTCCCTGGATGGCAAAATGCTCCATC	CAGCTGGATGATGATAGACATGGATTTGTTACCT		2601
OY	2699	CATAGACAATTAATGATTTTATTTTGGTGT	CGTGAAGACTACACACAGACTGGAGACTTTT		2758
Db	2602	CATAGACAATTAATGATTTTATTTTGGTGT	CGTGAAGACTACACACAGACTGGAGACTTTT		2661
OY	2759	TGGGACATCGAGGAGACTGTGATGAACAA	TTGCTTAACAATGGCGTCTTTAAAGAAT		2818
Db	2662	TGGGACATCGAGGAGACTGTGATGAACAA	TTGCTTAACAATGGCGTCTTTAAAGAAT		2721
OY	2819	TACCCCTTATGACTACCAAGCAGCATGTGT	AGGCCACACAGAAAGCAGCATGGCGGCCA		2878
Db	2722	TACCCCTTATGACTACCAAGCAGCATGTGT	AGGCCACACAGAAAGCAGCATGGCGGCCA		2781
OY	2879	TGGCCTCTGGATCCCTTATTAATGCTTTC	CTCTCGCAGTAAATGATTCATGACAGAACT		2938
Db	2782	TGGCCTCTGGATCCCTTATTAATGCTTTC	CTCTCGCAGTAAATGATTCATGACAGAACT		2841
OY	2939	TGTCTTGTTCCTGGTGGAAATTTAACTCT	CTGACAGTGGTGCACCTCGATATGACAGCTAA		2998
Db	2842	TGTCTTGTTCCTGGTGGAAATTTAACTCT	CTGACAGTGGTGCACCTCGATATGACAGCTAA		2901
OY	2999	AGCCCAAGAAATTTGAACAGACAGCCCTG	GGACCTTGATGATCAATATCCACATTCCTCTC		3058
Db	2902	AGCCCAAGAAATTTGAACAGACAGCCCTG	GGACCTTGATGATCAATATCCACATTCCTCTC		2961
OY	3059	TGAGCGCACCATCATCAAGGAGACTACAG	GGAATATTGCTTGGAAGACTGCTCCAAAGTCTT		3118
Db	2962	TGAGCGCACCATCATCAAGGAGACTACAG	GGAATATTGCTTGGAAGACTGCTCCAAAGTCTT		3021
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Db	3022	TGTCAATCCAGCAAAATCCCAAGCAGCA	CAACTGTTCATGTGTGTGTGGACAGCAGCTGCCT		3081
OY	3179	CTGTGATCTGTGGCCCCCATCCATCACT	ATGGACACCATTTGAAATCAGATTAATGAATCCCT		3238
Db	3082	CTGTGATCTGTGGCCCCCATCCATCACT	ATGGACACCATTTGAAATCAGATTAATGAATCCCT		3141
OY	3239	TAAGTGTGAACGTCTAAAGGCCCAGAAG	ATCACAGAGCGGCCAGAAATCTTGTATGGCTT		3298
Db	3142	TAAGTGTGAACGTCTAAAGGCCCAGAAG	ATCACAGAGCGGCCAGAAATCTTGTATGGCTT		3201
OY	3299	CCATCCCTGAGGAGAAATGCAAGGAGAGT	GTGGGGTGGCGGAGTCTTCCAAGCCACGACGT		3358
Db	3202	CCATCCCTGAGGAGAAATGCAAGGAGAGT	GTGGGGTGGCGGAGTCTTCCAAGCCACGACGT		3261
OY	3359	CCCTCTTCTGCACCCCTCTCTTTTGTAT	GTGCTTCTCAAGGTGCATCTGACTAGATGTTT		3418
Db	3262	CCCTCTTCTGCACCCCTCTCTTTTGTAT	GTGCTTCTCAAGGTGCATCTGACTAGATGTTT		3321
OY	3419	TCTTACTGACTAGATGTTTCTCTTGGCAT	GTCTAAATCATGAGATTAACACTGGAACCAAAAT		3478
Db	3322	TCTTACTGACTAGATGTTTCTCTTGGCAT	GTCTAAATCATGAGATTAACACTGGAACCAAAAT		3381
OY	3479	ATGGGTGCACAATACGAGACATGAATATAT	AGTCCAAACCATCAGCATCTCATCATGATTTTAA		3538
Db	3382	ATGGGTGCACAATACGAGACATGAATATAT	AGTCCAAACCATCAGCATCTCATCATGATTTTAA		3441
OY	3539	ACTGTGCGGTGATATTAACGTCTTAAAG	AGATATGTGTGACAAAAGTTATCTATCATCTTTTAA		3598
Db	3442	ACTGTGCGGTGATATTAACGTCTTAAAG	AGATATGTGTGTGACAAAAGTTATCTATCATCTTTTAA		3501
OY	3599	CTTTTGCAGTCAATGCAAAATGTGAGTTT	TGCCACATATATATCAACCTTATCAAGAAATGGG		3658
Db	3502	CTTTTGCAGTCAATGCAAAATGTGAGTTT	TGCCACATATATATCAACCTTATCAAGAAATGGG		3561
OY	3659	ACCGCAAGTGGTAGGCAAGTGTCCCTT	CTGTGATGAACCACTATTTGAACCAATTTAAACTG		3718

Db 3562 ACCGCAATGGTAGCGAGTGCCTTGTGCTTAACCACTATTGAACCACTTTAAACTG 3621

Qy 3719 TGTACTTTTAAATAAAGTATATTAAAAATCATAAAAA 3770

Db 3622 TGTACTTTTAAATAAAGTATATTAAAAATCATAAAAA 3673

```

RESULT 5
AAA09261
ID   AAA09261 standard; cDNA; 3598 BP.

```

AC AAAA09261;

DT 10-AUG-2000 (first entry)

Human alpha-2-delta-C gene splice variant.

KW alpha-2-delta-C; calcium channel subunit, 3p21.1; gabapentin; cyostatic;  
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant;  
KW

KW splice variant; ss.

OS Homo sapiens.

PN WO200020450-A2.

PD 13-APR-2000.

PF 07-OCT-1999; 99WO-US23519.

PR 07-OCT-1998; 98US-0103322.

PR 29-DEC-1998; 98US-0114088.

PA (WARN ) WARNER LAMBERT CO.

PI Johns MA, Moldover B, Offord JD;

DR WPI; 2000-303744/26.

PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D  
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,  
PT anxiety, multiple sclerosis or cancer

PS Claim 22; Page 85-86; 88pp; English.

CC The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.  
CC  
CC The alpha-2-delta-C gene is mapped to chromosome 3p21.1. This gene and the related  
CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells  
CC from abnormal calcium flux by introducing expression vectors containing  
CC the respective gene into mammalian cells. The antisense genes are also  
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein  
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.  
CC Therefore, alpha-delta-2 proteins may also be targeted to treat  
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic  
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),  
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or  
CC addiction syndromes, mood, depression or cancer.

Sequence 3598 BP; 1004 A; 836 C; 904 G; 853 T; 1 other;

Query Match	90.28;	Score 3399.2;	DB 21;	Length 3598;
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Matches	3594;	Conservative	0;	Mismatches	4;	Indels	172;	Gaps	2;
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2Y 1 TACTATAGGGCGCGCGAATTCGGCAGAGGGCGCGGAGCGGAGCAGGCGAGCCCCGC 60

Db 1 TACTATAGGCGCGCGAATTCGGCAGAGGCGCGCGGAGCGGAGCAGGACGCCCGC 60

61 GCGCTGCCACCGCCGCTCGCGCAGCTCCCGCGCGCGCTCTCGTCGCCCGCGCAGC 120

Db 61 GCGCTGCCACCGCGCTCCGGCAGCTCCCCGGCGCGCTCTGTGCGCCGCGCAGC 120

Db	1201	ACACACGGGACAAAGAGGTATCTGCAGTCAGCGCCATCATGCTCTAATCTATGATGGGGCGG	1266
Qy	1261	TGGACACCTATGATATCAATCTTTGCAAAATATCAATTTGGCCAGATCGAAAGGTTCCGACTCT	1320
Db	1261	TGGACACCTATGATATCAATCTTTGCAAAATATCAATTTGGCCAGATCGAAAGGTTCCGACTCT	1320
Qy	1321	TCACATACCTCATTTGGACGAGAGGCTGGTGTTCGACAAATCTAAAGTGAATGGCTGTG	1386
Db	1321	TCACATACCTCATTTGGACGAGAGGCTGGTGTTCGACAAATCTAAAGTGAATGGCTGTG	1386
Qy	1381	CCAAACAAAGATTTTTTATCCGAGATCTCCACCTTGGCTGATGTGGAGAGATGTCAATG	1444
Db	1381	CCAAACAAAGATTTTTTATCCGAGATCTCCACCTTGGCTGATGTGGAGAGATGTCAATG	1444
Qy	1441	AATATCTTACAGTGTCTAGCCGGCCAAAGTCATCGACACGAGCATGATGTGTGTGGA	1500
Db	1441	AATATCTTACAGTGTCTAGCCGGCCAAAGTCATCGACACGAGCATGATGTGTGTGGA	1500
Qy	1501	CCGAAAGCTTACATTGACAGCACTCGATGATGATCAGAGGCCGCTCTGATGACCATG	1560
Db	1501	CCGAAAGCTTACATTGACAGCACTCGATGATGATCAGAGGCCGCTCTGATGACCATG	1560
Qy	1561	TAGCCATGCTCTGTGTTTAGTAAAGCAAGCAAAACAGATCTCAAGGGCTTTCTTGGGAG	1620
Db	1561	TAGCCATGCTCTGTGTTTAGTAAAGCAAGCAAAACAGATCTCAAGGGCTTTCTTGGGAG	1620
Qy	1621	TGCTTTGGCACAGATGTCCCACTGTAAGAACTCTTGAAGACCATCCCAATATCAAGTTAG	1680
Db	1621	TGCTTTGGCACAGATGTCCCACTGTAAGAACTCTTGAAGACCATCCCAATATCAAGTTAG	1680
Qy	1681	GGATTTCACGGTATAGCCCTTGGCATTCACAAATATGATGATATCTTGAAGCATCCGGAAC	1740
Db	1681	GGATTTCACGGTATAGCCCTTGGCATTCACAAATATGATGATATCTTGAAGCATCCGGAAC	1740
Qy	1741	TCAGGCTGTCTATAGCAAGAAAGGAAAAAGCGAAGAAACCTATATAGTACGCTTGACC	1800
Db	1741	TCAGGCTGTCTATAGCAAGAAAGGAAAAAGCGAAGAAACCTATATAGTACGCTTGACC	1800
Qy	1801	TCCTCTAGAGGTGGAGTGGGAAACCCGAGATGACGTGTTGAGAAATGCTATGGTGAATCGAA	1860
Db	1801	TCCTCTAGAGGTGGAGTGGGAAACCCGAGATGACGTGTTGAGAAATGCTATGGTGAATCGAA	1860
Qy	1861	AGACGGGGAAGTTTCCATGAGAGGTGAAAGAACAGTGGACAAAGGGAACCGGTTTTGG	1920
Db	1861	AGACGGGGAAGTTTCCATGAGAGGTGAAAGAACAGTGGACAAAGGGAACCGGTTTTGG	1920
Qy	1921	TGATGACAAATGACTACTATTATATACAGACATCAAGGCTACTCTTGTAGTTAGGTTGG	1980
Db	1921	TGATGACAAATGACTACTATTATATACAGACATCAAGGCTACTCTTGTAGTTAGGTTGG	1980
Qy	1981	CGCTTTCCAGAGGTCAATGGGAAATATTTCTTCCGAGGGAATGTATACCATCGAAGAGGCC	2040
Db	1981	CGCTTTCCAGAGGTCAATGGGAAATATTTCTTCCGAGGGAATGTATACCATCGAAGAGGCC	2040
Qy	2041	TGCATGACTTAGAACAATCCGAGATGTCTCTTGGCAATGATGTCTTACTGCAACACTG	2100
Db	2041	TGCATGACTTAGAACAATCCGAGATGTCTCTTGGCAATGATGTCTTACTGCAACACTG	2100
Qy	2101	ACCTACACCTTGACACCGCATCTGTCTACGTTAGAGGATTAAGCTTACTTAAAG	2160
Db	2101	ACCTACACCTTGACACCGCATCTGTCTACGTTAGAGGATTAAGCTTACTTAAAG	2160
Qy	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGTATCCAAAGATCTTTTGTGACGGG	2220
Db	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGTATCCAAAGATCTTTTGTGACGGG	2220
Qy	2221	TGGTGAAGTCCCCCATTTGAAGCGTATTTGACCAAGCTGTGGCCCTCAACAATCTGAAATTT	2280
Db	2221	TGGTGAAGTCCCCCATTTGAAGCGTATTTGACCAAGCTGTGGCCCTCAACAATCTGAAATTT	2280
Qy	2281	CTGACAAAGGCGTGAAGTTGCTTCCTTCCGAGACTGACAGGGGCTCTCAGAAATCAAC	2340
Db	2281	CTGACAAAGGCGTGAAGTTGCTTCCTTCCGAGACTGACAGGGGCTCTCAGAAATCAAC	2340

[illegible]

Oy	3421	TTACGAGCAGATGTCTTCTTGCGATCGTAATCATGGATAAAGTCGAACCAAAATAT	3480
Db	3249	TTACTGACGAGATGTCTCTTGCGATCGTAATCATGGATMAACTGGAACCAAAATAT	3308
Oy	3481	GGTGCACAATACGAGACATGAATPATATGTCACCAACATCAGATCTCATCATGATTTTAAAC	3540
Db	3309	GGTGCACAATACGAGACATGAATPATATGTCACCAACATCAGATCTCATCATGATTTTAAAC	3368
Oy	3541	TGTGGCTGATPATAAAGTCTTAAAGATATGTGGACAAAAAGTTATCTATCATCTTTTACT	3600
Db	3369	TGTGGCTGATPATAAAGTCTTAAAGATATGTGGACAAAAAGTTATCTATCATCTTTTACT	3428
Oy	3601	TTGCCAGTCATCCAATGTGAAGTTGGCCACATGATAATCACCTTCATCAGAAAATGGGAC	3660
Db	3429	TTGCCAGTCATCCAATGTGAAGTTGGCCACATGATAATCACCTTCATCAGAAAATGGGAC	3488
Oy	3661	CCCAAGTGTAGGCGAGTGTCCCTCTGCTTGAAACCTATTGAAACCAATTTTAAACTGTG	3720
Db	3489	CCCAAGTGTGTAGGCGAGTGTCCCTCTGCTTGAAACCTATTGAAACCAATTTTAAACTGTG	3548
Oy	3721	TACTTTTTTAATAGTATATTAATATATATAAAAAAAAAAAAAAAAAAAAAA	3770
Db	3549	TACTTTTTTAATAGTATATATTAATATATATAAAAAAAAAAAAAAAAAAAAAA	3598
 RESULT 6 AAS01409			
ID	AAS01409	standard; cDNA; 3213 BP.	
Xx	AAS01409;		
Ac	AAS01409;		
Xx			
Dt	04-JUL-2001	(first entry)	
Xx			
De	Human secreted soluble alpha2delta calcium channel subunit #6 cDNA.		
Xx			
Kw	Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;		
Kw	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;		
Kw	gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;		
Km	filter binding assay; wheat germ lectin flashplate assay; ss.		
Xx			
Os	Homo sapiens.		
Fh	Key	Location/Qualifiers	
Ft	CDS	1..3213	
Ft		/+tag= a	
Ft		/partial	
Ft		/product= "Alpha2delta calcium channel subunit #6"	
Ft		/note= "This sequence lacks a stop codon"	
Ft		/transl_except= (pos:3130..3153,aa:Arg-Arg)	
Ft		/note= "These two codons between them have an	
Ft		apparent 18 nucleotide insertion"	
Xx			
Rn	W0200119870-A2.		
Xx			
Pd	22-MAR-2001.		
Xx			
Pf	18-SEP-2000; 2000WO-EP09137.		
Xx			
Pr	16-SEP-1999; 99US-0397550.		
Xx			
Pa	(WARN ) WARNER LAMBERT CO.		
Xx			
Pi	Brown JP, Bertelli F;		
Xx			
Dr	WPI; 2001-235262/24.		
Dr	P-PsDB; AAD01019.		
Xx			
Pt	Calcium channel alpha2delta subunits, useful in e.g. SPA assays,		
Pt	wheat germ lectin flashplate assays, Filter binding assays or		
Xs	Claim 39; Page 71-72; 160pp; English.		







1944 ACAGACATCAAGGGTACTCCTTTTCAGTTTAGTGTGGCGCTTTCCAGAGTCATGGGAAA 2003  
1801 ACAGACATCAAGGGTACTCCTTTTCAGTTTAGTGTGGCGCTTTCCAGAGTCATGGGAAA 1860  
2004 TATTTCTTCGAGGGAATGTAAACCATCGAAGAGCCCTGCATGACTTGAACATCCGAT 2063  
1861 TATTTCTTCGAGGGAATGTAAACCATCGAAGAGCCCTGCATGACTTGAACATCCGAT 1920  
2064 GTGTCTTCGAGGGAATGTAAACCATCGAAGAGCCCTGCATGACTTGAACATCCGAT 2123  
1921 GTGTCTTCGAGGGAATGTAAACCATCGAAGAGCCCTGCATGACTTGAACATCCGAT 1980  
2124 CTGTCTTCGAGGGAATGTAAACCATCGAAGAGCCCTGCATGACTTGAACATCCGAT 2183  
1981 CTGTCTTCGAGGGAATGTAAACCATCGAAGAGCCCTGCATGACTTGAACATCCGAT 2040  
2184 GATTAAGAAATTTGATCCAAAGAGTCTTTTTCAGCGCGGTGGTGAAGTCCCATTTGAAGCG 2243  
2041 GATTAAGAAATTTGATCCAAAGAGTCTTTTTCAGCGCGGTGGTGAAGTCCCATTTGAAGCG 2100  
2244 TATTTGACACAGCTGGCGCTTCACAAATCTGAAATTTCTGACAAAGGCGTGGAGTTGCC 2303  
2101 TATTTGACACAGCTGGCGCTTCACAAATCTGAAATTTCTGACAAAGGCGTGGAGTTGCC 2160  
2304 TTTCTGCGACCTGGACAGGCGCTTCACAAATCTGAAATTTCTGACAAAGGCGTGGAGTTGCC 2363  
2161 TTTCTGCGACCTGGACAGGCGCTTCACAAATCTGAAATTTCTGACAAAGGCGTGGAGTTGCC 2220  
2364 ACCAATCAGACCTTTCTGAAAGTGGCGACAGAGAACATTTTTCAGAGACATTTTC 2423  
2221 ACCAATCAGACCTTTCTGAAAGTGGCGACAGAGAACATTTTTCAGAGACATTTTC 2280  
2424 CCTCTCTGACAGGAGAGCGCGCTTCAGAGATTTCCAGAGGCTTCTGATCTGATCCCA 2483  
2281 CCTCTCTGACAGGAGAGCGCGCTTCAGAGATTTCCAGAGGCTTCTGATCTGATCCCA 2340  
2484 TTTGAGCAGTGGACAGTCAATTAAGCAATGTGTGACAGCAAGTCAATCCATCCAGCTTC 2543  
2341 TTTGAGCAGTGGACAGTCAATTAAGCAATGTGTGACAGCAAGTCAATCCATCCAGCTTC 2400  
2544 CTGGATGAACGGAAATCTCTGTGTGGGACGTGTAGGCAATTCAGATGAACATTTGAATTT 2603  
2401 CTGGATGAACGGAAATCTCTGTGTGGGACGTGTAGGCAATTCAGATGAACATTTGAATTT 2460  
2604 TTTGCAAGGAAGTTCTGAGACTGCGACAGACAGTGTCTTCCCTGGATGGCAATCTCC 2663  
2461 TTTGCAAGGAAGTTCTGAGACTGCGACAGACAGTGTCTTCCCTGGATGGCAATCTCC 2520  
2664 ATCAGCTGTGATGATGAGACTGTGAATTTTACCTCATAGCAATTAATGATTTATTTTG 2723  
2521 ATCAGCTGTGATGATGAGACTGTGAATTTTACCTCATAGCAATTAATGATTTATTTTG 2580  
2724 GTGTCTGAAGACTACACAGACTGGAGACTTTTGTGTGAGATCGAGGAGCTGTGATG 2783  
2581 GTGTCTGAAGACTACACAGACTGGAGACTTTTGTGTGAGATCGAGGAGCTGTGATG 2640  
2784 AACCAATTCCTAAACATGGGCTCTTTTAAACAAATTTACCTTTATGACTACCAAGCCATG 2843  
2641 AACCAATTCCTAAACATGGGCTCTTTTAAACAAATTTACCTTTATGACTACCAAGCCATG 2700  
2844 TGTAGAGCCAAACAGAAAGCAGCGATGGCGCCATGGCTCTGGATTCCTTATATATGCG 2903  
2701 TGTAGAGCCAAACAGAAAGCAGCGATGGCGCCATGGCTCTGGATTCCTTATATATGCG 2760  
2904 TTTCTCTCTGAGTAAATGATGATGACAGAACTTGTCTTCTGCTGGTGAATTTAAC 2963  
2761 TTTCTCTCTGAGTAAATGATGATGACAGAACTTGTCTTCTGCTGGTGAATTTAAC 2820  
2964 CTCTGCAATTTGGTGGCAGTCCGATATGACAGCTTAAAGCCCAAAATTTGAACAGACCTTC 3023  
2821 CTCTGCAATTTGGTGGCAGTCCGATATGACAGCTTAAAGCCCAAAATTTGAACAGACCTTC 2880

3024 GAGCCTTGTGATGATGATATCCAGCATTTGCTCTGACGGCGACCATTCAGAGACTTACA 3083  
2881 GAGCCTTGTGATGATGATATCCAGCATTTGCTCTGACGGCGACCATTCAGAGACTTACA 2940  
3084 GCGAATATTCCTTGTGAAGACTGCTCAAGTCTTTTTCATCCAGCAAAATCCCAAGCAGC 3143  
2941 GCGAATATTCCTTGTGAAGACTGCTCAAGTCTTTTTCATCCAGCAAAATCCCAAGCAGC 3000  
3144 AACCTTTTCATGTTGTGTGTGACAGAGTGCCTCTGTGAATTCGTGGCCCATCACC 3203  
3001 AACCTTTTCATGTTGTGTGTGACAGAGTGCCTCTGTGAATTCGTGGCCCATCACC 3060  
3204 ATGGCACCCTTTGAATCAGATATTAATGATTCCTTTAAGTGTGACGCTTAAA----- 3256  
3061 ATGGCACCCTTTGAATCAGATATTAATGATTCCTTTAAGTGTGACGCTTAAAAGGCCAG 3120  
3257 -----GGCCCAAGATCAGAAAGCGCCACAGATCTTGTGATGAGCTTCAATCCT 3305  
3121 AAGATCAGAAAGGCCCAAGATCAGAAAGCGCCACAGATCTTGTGATGAGCTTCAATCCT 3180  
3306 GAGGAGAAATCAGAGGAGTGTGGGGTGCAGC 3338  
3181 GAGGAGAAATCAGAGGAGTGTGGGGTGCAGC 3213  
RESULT 7  
AAF57546  
ID AAF57546 standard; DNA; 3213 BP.  
XX  
XX AAF57546;  
AC  
XX  
DT 11-JUN-2001 (first entry)  
XX  
XX Human calcium channel alpha2delta subunit encoding DNA.  
DE  
XX  
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.  
OS  
XX Homo sapiens.  
OS  
PN W0200120336-A2.  
XX  
PD 22-MAR-2001.  
XX  
PE 18-SEP-2000; 2000MO-EP09136.  
XX  
PR 16-SEP-1999; 99US-0397549.  
XX  
PA (WARN ) WARNER LAMBERT CO.  
XX  
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
PI WPI: 2001-257902/26.  
DR P-PSDB: AAB62243.  
XX  
PT Competitive binding assay for screening ligands which bind a cerebral  
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
PT where the ligands identified are useful for treating disorders of the  
PT nervous system, including pain -  
XX  
XX  
PS Disclosure: Page 71-72; 158pp; English.  
XX  
XX The invention relates to a new method for screening ligands which bind a  
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
CC preferably alpha2delta-1 subunit. The method comprises contacting a  
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
CC interest and a labelled compound which binds the subunit, followed by  
CC measuring the level of binding of the labelled compound to alpha2delta-1  
CC subunit. The method is useful for screening ligands, preferably  
CC biologically active products that modulate a nervous system function,  
CC which bind a cerebral cortical voltage-dependent calcium channel  
CC alpha2delta-1 subunit. The ligands identified by the method are useful  
CC for treating disorders of the nervous system, including pain, epilepsy



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Db 2041 GATAAAGATTGATCCAGAGAGTCTTTTGTGACGGGGTGTGAGTGGCCCATTTAAACG 2100
Oy 2244 TATTGGACACCTGGCCCTTAACAAATCTGAAAAATTTGTACAGAGGGCTGGAGTTGCC 2303
Db 2101 TATTGGACACCTGGCCCTTAACAAATCTGAAAAATTTGTACAGAGGGCTGGAGTTGCC 2160
Oy 2304 TTCTCGCAGCTGCGACGGGCTCTCCAGAAATCAACCTGTTGTGGGGCTGAGACGCTC 2363
Db 2161 TTCTCGCAGCTGCGACGGGCTCTCCAGAAATCAACCTGTTGTGGGGCTGAGACGCTC 2220
Oy 2364 ACCAATCAGACCTTCTGAAAGCTGGGACAAAGAAACATTTTAAACGACCATTTTC 2280
Db 2221 ACCAATCAGACCTTCTGAAAGCTGGGACAAAGAAACATTTTAAACGACCATTTTC 2280
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Db 2281 CCCTCTGCTGTAACCGAAGACGGCTGAGACAGTTCCAGGAGCTTCTCTACTCATCCCA 2340
Oy 2484 TTACGACCTGGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2543
Db 2341 TTACGACCTGGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2400
Oy 2544 CTGGATGAACGGAATCTCTGTGTGTGGAGCTGTAGGCAATTCAGTGAATTTGAATTT 2603
Db 2401 CTGGATGAACGGAATCTCTGTGTGTGGAGCTGTAGGCAATTCAGTGAATTTGAATTT 2460
Oy 2604 TTCCAAAGGAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2663
Db 2461 TTCCAAAGGAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
Oy 2664 ATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2723
Db 2521 ATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
Oy 2724 GTGTCTGAGACTACACACAGACTGGAGACTTTTGGTGTGAGATTCAGGAGCTGTGATG 2783
Db 2581 GTGTCTGAGACTACACACAGACTGGAGACTTTTGGTGTGAGATTCAGGAGCTGTGATG 2640
Oy 2784 AACAAATTTGCTAACATTTGGCTCTTAAAGAAATTAACCTTTATGACTACCAAGCCATG 2843
Db 2641 AACAAATTTGCTAACATTTGGCTCTTAAAGAAATTAACCTTTATGACTACCAAGCCATG 2700
Oy 2844 TGTAGAGCCAAAGAAAGACGATGGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2903
Db 2701 TGTAGAGCCAAAGAAAGACGATGGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Oy 2904 TTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2963
Db 2761 TTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
Oy 2964 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3023
Db 2821 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Oy 3024 GAGCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3083
Db 2881 GAGCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
Oy 3084 GGAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3143
Db 2941 GGAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
Oy 3144 AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3203
Db 3001 AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
Oy 3204 ATGCAACCATTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3256
Db 3061 ATGCAACCATTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
Oy 3257 -----GGCCCAAGATCAGAAAGGCGCCAGATCTTGTGATGCTTCCATCT 3305
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Db 3121 AAGATCAGAGAGGCGCCAGACATCAGAGGCGCCAGATCTTGTATGCTTCATCT 3180
Oy 3306 GAGGAGAAATGCAAGGAGCTGTGGGTGCGCCG 3338
Db 3181 GAGGAGAAATGCAAGGAGCTGTGGGTGCGCCG 3213

RESULT 8
AAS01408
ID AAS01408 standard; cDNA; 3114 BP.
XX
AC AAS01408;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #5 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 1..3114
FT /tag- a
FT /partial
FT /product- "Alpha2delta calcium channel subunit #5"
FT /note- "this sequence lacks a stop codon"
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000MO-EP09137.
XX
PR 16-SEP-1999; 99US-0397550.
XX
PA (WARN ) WARNER LAMBERT. CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI: 2001-235262/24.
DR P-PSDB: AAU01018.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays.
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT wheat germ lectin flashplate assays -
XX
PS Claim 39; Page 70-71; 160pp; English.
XX
CC The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #5 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labeled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
CC described. The secreted soluble alpha2delta subunit may be used in assays
CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-leucine, L-Allo-leucine, L-methionine, L-leucine, L-isoleucine,
CC L-valine, spermine and/or L-phenylalanine) of a calcium channel
CC alpha2delta subunit.
XX
Sequence 3114 BP; 868 A; 704 C; 789 G; 752 T; 1 other:

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Db 2101 TATGACACAGCCTGGCCCTCAACAATCTGAAATTTCTGCAAGGGCGGTGAGAGTTGCC 2160
Qy 2304 TTCTCGGCACTGCCAGGGGCTCTCCAGATCAACCTGTTTGGGGGCTGAGCAGCTC 2363
Db 2161 TTCTCGGCACTGCCAGGGGCTCTCCAGATCAACCTGTTTGGGGGCTGAGCAGCTC 2220
Qy 2364 ACCAATGAGACTCTCTGAAAGCTGGGACACAAAGAACTTTTAAACGCGAGCACTTTC 2423
Db 2221 ACCAATGAGACTCTCTGAAAGCTGGGACACAAAGAACTTTTAAACGCGAGCACTTTC 2280
Qy 2424 CCTCTGTGATACGAGAGCGGCTGAGCAGATTTCAGGAGCTTCTCTACTGATCCCA 2483
Db 2281 CCTCTGTGATACGAGAGCGGCTGAGCAGATTTCAGGAGCTTCTCTACTGATCCCA 2340
Qy 2484 TTGAGCACTGAGCAGCACTCAATTAAGCAATGTGTGACAGCAAGTACATCCACCTC 2543
Db 2341 TTGAGCACTGAGCAGCACTCAATTAAGCAATGTGTGACAGCAAGTACATCCACCTC 2400
Qy 2544 CTGGATGACGGAATCTCTGTGTGGGACGCTGTAGCAATTCAGATGAACCTTGAATTT 2603
Db 2401 CTGGATGACGGAATCTCTGTGTGGGACGCTGTAGCAATTCAGATGAACCTTGAATTT 2460
Qy 2604 TTCCAAAGAACTTCTGAGCTGCCAGCAGACAGTGTGCTTCCCTGATGCGCAATGCTCC 2663
Db 2461 TTCCAAAGAACTTCTGAGCTGCCAGCAGACAGTGTGCTTCCCTGATGCGCAATGCTCC 2520
Qy 2664 ATGAGCTGTGATGATGAGACTGTGAAATTTGTACTCTCATACAAATTAATGATTTATTTG 2723
Db 2521 ATGAGCTGTGATGATGAGACTGTGAAATTTGTACTCTCATACAAATTAATGATTTATTTG 2580
Qy 2724 GTCTGTGAAGACTACACAGACTGTGAGACTTTTGGTGAGATCGAGGAGCGTGATG 2783
Db 2581 GTCTGTGAAGACTACACAGACTGTGAGACTTTTGGTGAGATCGAGGAGCGTGATG 2640
Qy 2784 AACAAATGCTAACAATGGGCTCTTTAAAGAAATTAACCTTTATGACTACCAAGCAT 2843
Db 2641 AACAAATGCTAACAATGGGCTCTTTAAAGAAATTAACCTTTATGACTACCAAGCAT 2700
Qy 2844 TGTAGAGCCAAACAAGAAAGACAGATGGCGCCATGGCTCTCTGATCTTATATGTC 2903
Db 2701 TGTAGAGCCAAACAAGAAAGACAGATGGCGCCATGGCTCTCTGATCTTATATGTC 2760
Qy 2904 TTCTCTCTGAGTAAATAGATCATGACAGAACTTGTGTTCCGGGTGAATTAAC 2963
Db 2761 TTCTCTCTGAGTAAATAGATCATGACAGAACTTGTGTTCCGGGTGAATTAAC 2820
Qy 2964 CTCTGCAAGTTGGTGACATCCGATATGACAGCTAAAGCCAGAAATTTGAACAGACCTG 3023
Db 2821 CTCTGCAAGTTGGTGACATCCGATATGACAGCTAAAGCCAGAAATTTGAACAGACCTG 2880
Qy 3024 GAGCCTGTGATACGTAATNTCCAGCATTCGCTCTGAGCGCCACCTCAAGAGACTACA 3083
Db 2881 GAGCCTGTGATACGTAATNTCCAGCATTCGCTCTGAGCGCCACCTCAAGAGACTACA 2940
Qy 3084 GGGAAATATTTGCTGTCAAGACTGCTCAAGTCTTGTCTCATCCAGCAATTCACACAGC 3143
Db 2941 GGGAAATATTTGCTGTCAAGACTGCTCAAGTCTTGTCTCATCCAGCAATTCACACAGC 3000
Qy 3144 AACCTGTTTATGTTGGTGTGACAGACAGCTGCTGTGAAATCTGTGGCCGCCATCAC 3203
Db 3001 AACCTGTTTATGTTGGTGTGACAGACAGCTGCTGTGAAATCTGTGGCCGCCATCAC 3060
Qy 3204 ATGGACACCATTAATGATGATTAATGATCCCTTAAGTGTGAACGTTAAAG 3257
Db 3061 ATGGACACCATTAATGATGATTAATGATCCCTTAAGTGTGAACGTTAAAG 3114

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RESULT 9  
 AAF57545  
 ID AAF57545 standard: DNA: 3114 BP.  
 XX  
 AC AAF57545;

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XX 11-JUN-2001 (first entry)
DT
XX Human calcium channel alpha2delta subunit encoding DNA.
DE
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..3114
FT CDS /+tag- a
FT
XX
XX W0200120336-A2.
XX
XX 22-MAR-2001.
XX
XX 18-SEP-2000; 2000MO-EP09136.
XX
XX 16-SEP-1999; 9905-0397549.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX WPI: 2001-257902/26.
XX
XX P-PSDB: AAB62242.
XX
XX Competitive binding assay for screening ligands which bind a cerebral
XX cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
XX where the ligands identified are useful for treating disorders of the
XX nervous system, including pain -
XX
XX Disclosure: Page 70-71; 158pp; English.
XX
XX The invention relates to a new method for screening ligands which bind a
XX cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
XX preferably alpha2delta-1 subunit. The method comprises contacting a
XX secreted soluble recombinant alpha2delta-1 subunit with a ligand of
XX interest and a labelled compound which binds the subunit, followed by
XX measuring the level of binding of the labelled compound to alpha2delta-1
XX subunit. The method is useful for screening ligands, preferably
XX biologically active products that modulate a nervous system function,
XX which bind a cerebral cortical voltage-dependent calcium channel
XX alpha2delta-1 subunit. The ligands identified by the method are useful
XX for treating disorders of the nervous system, including pain, epilepsy
XX and anxiety. The present sequence represents a human calcium channel
XX alpha2delta subunit encoding DNA.
XX
XX Sequence 3114 BP; 868 A; 704 C; 789 G; 752 T; 1 other:
SQ
Query Match 82.6%; Score 3113.6; DB 22; Length 3114;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 144 ATGGCCGGGCGGGCTGCGCGCGCGCGCGCGGGGCGCTGCGCGCTTCTGCTGCC 203
Db 1 ATGGCCGGGCGGGCTGCGCGCGCGCGCGCGCGGGGCGCTGCGCGCTTCTGCTGCC 60
Qy 204 GCGCTTCTACGCGCGCTGGGGGACGTGTGCGCTCGGAGCAGCATACCGCTTCC 263
Db 61 GCGCTTCTACGCGCGCTGGGGGACGTGTGCGCTCGGAGCAGCATACCGCTTCC 120
Qy 264 GTGTGAAGCTCTGCGCTTGTGGTGAGATTAATCCATGCTGCTAAGTAC 323
Db 121 GTGTGAAGCTCTGCGCTTGTGGTGAGATTAATCCATGCTGCTAAGTAC 180
Qy 324 TCCGCTCCAGCTTCTCAAAAGAAATACAAAGATATGAGAAAGAGCTTGCCTAGAA 383
Db 181 TCCGCTCCAGCTTCTCAAAAGAAATACAAAGATATGAGAAAGAGCTTGCCTAGAA 240
Qy 384 GAAATTAATGAGCTTCAACCTGTGTAAGAAAGCTGGCAAAAGAAATGGAAGATGTTTAC 443

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Db 241 GAAATGATGGCTCCAAAGCTGAAGAAAGCTGGCAAGAAACATGGAAGATGTTTCAC 300  
QY 444 AAGAAGCTGAGGCGGTCAGGCGCTGTGGAGGCTGCAGAAAGACACACACCTGAAACAT 503  
|||||  
Db 301 AAGAAGCTGAGGCGGTCAGGCGCTGTGGAGGCTGCAGAAAGACACACCTGAAACAT 360  
QY 504 GAATTTGATGCAGACTTACAGTATGATGATTAATCTGATGCTGTGATTAATGAAAGGAC 563  
|||||  
Db 361 GAATTTGATGCAGACTTACAGTATGATGATTAATCTGATGCTGTGATTAATGAAAGGAC 420  
QY 564 AAGAGGCGGAATTTTGGAGCTGGGAAAGAAATTCATCTTAAAGCCCAATGACCATTTT 623  
|||||  
Db 421 AAGAGGCGGAATTTTGGAGCTGGGAAAGAAATTCATCTTAAAGCCCAATGACCATTTT 480  
QY 624 AATAATTTGCTGTGAACATCACTTAAGTGAAGTCCAACTACCAAGCAATGTACAC 683  
|||||  
Db 481 AATAATTTGCTGTGAACATCACTTAAGTGAAGTCCAACTACCAAGCAATGTACAC 540  
QY 684 AAGACCCCTGCAATTTGCAATGAGGCTTATTTGCTGAATCTGTAACCAAGTTTGTGA 743  
|||||  
Db 541 AAGACCCCTGCAATTTGCAATGAGGCTTATTTGCTGAATCTGTAACCAAGTTTGTGA 600  
QY 744 GATACCTTTGACCGTGAACCATCTCATATGAGCAGTACTTTGGAAGTGCMAAGGCTTT 803  
|||||  
Db 601 GATACCTTTGACCGTGAACCATCTCATATGAGCAGTACTTTGGAAGTGCMAAGGCTTT 660  
QY 804 TTTAGGCAATTCGCGGGGATTAATGAGAACCGAGATGAGATGAGTCAATGCTTCGAC 863  
|||||  
Db 661 TTTAGGCAATTCGCGGGGATTAATGAGAACCGAGATGAGATGAGTCAATGCTTCGAC 720  
QY 864 TGCAGGAACCGAAATGATACATCCAGGAGCAACTTCCGAAAGACCGTGCATTTTA 923  
|||||  
Db 721 TGCAGGAACCGAAATGATACATCCAGGAGCAACTTCCGAAAGACCGTGCATTTTA 780  
QY 924 GTTGACGTAGTGGAGCATGAAAGGACTCGTCTGACTATCGCGAAGCAACAGTCTCA 983  
|||||  
Db 781 GTTGACGTAGTGGAGCATGAAAGGACTCGTCTGACTATCGCGAAGCAACAGTCTCA 840  
QY 984 TCCATTTTGGATACATTTGGGAGTGAATGATCTTCAACATATTTCTTATATGAGGAG 1043  
|||||  
Db 841 TCCATTTTGGATACATTTGGGAGTGAATGATCTTCAACATATTTCTTATATGAGGAG 900  
QY 1044 CTTCACATATGTGAACCTTGCCTGAATGGAATTTGGTGCAGACCGCAGCAACAA 1103  
|||||  
Db 901 CTTCACATATGTGAACCTTGCCTGAATGGAATTTGGTGCAGACCGCAGCAACAA 960  
QY 1104 GAGCACTTCAGGAGCATCTGACAAACTTTTCGCCAAAGGAATTTGGATATA 1163  
|||||  
Db 961 GAGCACTTCAGGAGCATCTGACAAACTTTTCGCCAAAGGAATTTGGATATA 1020  
QY 1164 GCTCGAATGAGGCGCTTCAACATTTCTGAGTGAATTTCAACACGCGGACAAAGAGTATC 1223  
|||||  
Db 1021 GCTCGAATGAGGCGCTTCAACATTTCTGAGTGAATTTCAACACGCGGACAAAGAGTATC 1080  
QY 1224 TGCATCTAGGCGCATCTCATACTATGATGGGCGGTGGAGACCTATGATCAATCTTT 1283  
|||||  
Db 1081 TGCATCTAGGCGCATCTCATACTATGATGGGCGGTGGAGACCTATGATCAATCTTT 1140  
QY 1284 GCAAAATTCATTTGGCCAGATCGAAAGGTTGCGATCTTCACATACCTCAATTTGGAGAG 1343  
|||||  
Db 1141 GCAAAATTCATTTGGCCAGATCGAAAGGTTGCGATCTTCACATACCTCAATTTGGAGAG 1200  
QY 1344 GCTGCGTTTGGAGCAATCAATTAAGTGAATGAGTGCCTGTCGCAACAAAGAT TTTTATCCAG 1403  
|||||  
Db 1201 GCTGCGTTTGGAGCAATCAATTAAGTGAATGAGTGCCTGTCGCAACAAAGAT TTTTATCCAG 1260  
QY 1404 ATCTCCACCTTGGCTGATGTGAGAGAAATGTCAATGAATACCTTCAGTGTGTCGCGG 1463  
|||||  
Db 1261 ATCTCCACCTTGGCTGATGTGAGAGAAATGTCAATGAATACCTTCAGTGTGTCGCGG 1320  
QY 1464 CCGAAAGTCATCGACACGAGCATGATGTGTGTGAGCCGAAGCTTACATTTGACAGCACT 1523  
|||||

Db 1321 CCCAAAGTCATGACACGAGCATGATGTGTGTGAGCCGAGCTTACATTTGACAGCACT 1380  
QY 1524 CTGACTATGATACAGGCGCCCGTCTGATGACACCTGTAGCCATGCTGTGTTTAAAG 1583  
|||||  
Db 1381 CTGACTATGATACAGGCGCCCGTCTGATGACACCTGTAGCCATGCTGTGTTTAAAG 1440  
QY 1584 CAGAAAGAAACCATGAGAGGCGATCTTCTGGAGTGTGTGGCACAGATGTCCAGTG 1643  
|||||  
Db 1441 CAGAAAGAAACCATGAGAGGCGATCTTCTGGAGTGTGTGGCACAGATGTCCAGTG 1500  
QY 1644 AAGAACTTCTGAAGACATCCCAATACAGTTAGGATTCACGCTTATGCTTTGCA 1703  
|||||  
Db 1501 AAGAACTTCTGAAGACATCCCAATACAGTTAGGATTCACGCTTATGCTTTGCA 1560  
QY 1704 ATCACAATTAATGATATCTGACACATCCGAACTCAGGCTGTGTACGAAGAAGA 1763  
|||||  
Db 1561 ATCACAATTAATGATATCTGACACATCCGAACTCAGGCTGTGTACGAAGAAGA 1620  
QY 1764 AAAAAGGGAAGAAACCTAATAGTACGCTTCTCTGAGTGTGAGTGGAAAGAC 1823  
|||||  
Db 1621 AAAAAGGGAAGAAACCTAATAGTACGCTTCTCTGAGTGTGAGTGGAAAGAC 1680  
QY 1824 CGAATGACGCTTGAAGAAATGCTATGATGAAATCGAAAGACGGGAAAGTTTCCATGAG 1883  
|||||  
Db 1681 CGAATGACGCTTGAAGAAATGCTATGATGAAATCGAAAGACGGGAAAGTTTCCATGAG 1740  
QY 1884 GTGAAGAAAGACATGAGCAAGGAAACGGGTTTGTGTGATGCAAAATGACTATAT 1943  
|||||  
Db 1741 GTGAAGAAAGACATGAGCAAGGAAACGGGTTTGTGTGATGCAAAATGACTATAT 1800  
QY 1944 ACAGACATCAAGGCTACTCTTTCAGTTTATGTTGTGCGCTTTCAGAGTCAATGGAAA 2003  
|||||  
Db 1801 ACAGACATCAAGGCTACTCTTTCAGTTTATGTTGTGCGCTTTCAGAGTCAATGGAAA 1860  
QY 2004 TATTTCTCCGAGGATGTAATACATGGAAGAGGCTGATGACTTAAGCAATCCCGAT 2063  
|||||  
Db 1861 TATTTCTCCGAGGATGTAATACATGGAAGAGGCTGATGACTTAAGCAATCCCGAT 1920  
QY 2064 GTGTCTTGGCAGATGAATGCTCTACTGCAACATGACCTACACCTGAGCACCGCAT 2123  
|||||  
Db 1921 GTGTCTTGGCAGATGAATGCTCTACTGCAACATGACCTACACCTGAGCACCGCAT 1980  
QY 2124 CTGTCTCAGTTAGAACGATTAAGCTCTCAATTAAGCAAGAAAGACCTGCTCAAGTGT 2183  
|||||  
Db 1981 CTGTCTCAGTTAGAACGATTAAGCTCTCAATTAAGCAAGAAAGACCTGCTCAAGTGT 2040  
QY 2184 GATTAAGAAATTTGCAAGAGAGCTTTTGAACGGGCTGTGAGTGTGCTCCATGAAAGG 2243  
|||||  
Db 2041 GATTAAGAAATTTGCAAGAGAGCTTTTGAACGGGCTGTGAGTGTGCTCCATGAAAGG 2100  
QY 2244 TATTTGACAGGCTGTGCGCTTCAACAAATCTGAAATTTGCAAGAGGCGTGAAGTGGC 2303  
|||||  
Db 2101 TATTTGACAGGCTGTGCGCTTCAACAAATCTGAAATTTGCAAGAGGCGTGAAGTGGC 2160  
QY 2304 TTTCTCGGCACTGCGACGCGGCTGTCCAGATCAACCTGTTGTGTGGGCTGAGCAGCTC 2363  
|||||  
Db 2161 TTTCTCGGCACTGCGACGCGGCTGTCCAGATCAACCTGTTGTGTGGGCTGAGCAGCTC 2220  
QY 2364 ACCAATCAGAGTCTCTGAAACCTGGCGACAGGAAACATTTTAAACGCAACCATTTTC 2423  
|||||  
Db 2221 ACCAATCAGAGTCTCTGAAACCTGGCGACAGGAAACATTTTAAACGCAACCATTTTC 2280  
QY 2424 CCTCTCTGTGTACGGAAGACCGCTGAGAGATTTCCAGGAGCTTGTGTATCTCATCCCA 2483  
|||||  
Db 2281 CCTCTCTGTGTACGGAAGACCGCTGAGAGATTTCCAGGAGCTTGTGTATCTCATCCCA 2340  
QY 2484 TTTACACATCTGAGACGATCAATTAAGCAATGTGTGTGACAGCAAGTATCCATCCAGCTC 2543  
|||||  
Db 2341 TTTACACATCTGAGACGATCAATTAAGCAATGTGTGTGACAGCAAGTATCCATCCAGCTC 2400  
QY 2544 CTGATGAAAGCAATTCCTGTTGTGTGAGCTGTGAGGCAATTCAGATGAACCTGAATTT 2603  
|||||  
Db 2401 CTGATGAAAGCAATTCCTGTTGTGTGAGCTGTGAGGCAATTCAGATGAACCTGAATTT 2460

OY	2604	TTCCAAAGAAGATTCTGAGCTGCCAGACAGACAGTGTGCTTCCCTGGATGGCAATGCTCC	2663
Db	2461	TTCCAAAGAAGATTCTGAGCTGCCAGACAGTGTGCTTCCCTGGATGGCAATGCTCC	2520
OY	2664	ATCAGCTGTATGATGAGACTGTGAATTTGTTACCTCATAGACAAATAATGGATTTATTTTG	2723
Db	2521	ATCAGCTGTATGATGAGACTGTGAATTTGTTACCTCATAGACAAATAATGGATTTATTTTG	2580
OY	2724	GTGTCTGAAGACTACACAGACAGCTGAGACTTTTGTGGTGAATCGAGGGAGCTGTGATG	2783
Db	2581	GTGTCTGAAGACTACACAGACAGCTGAGACTTTTGTGGTGAATCGAGGGAGCTGTGATG	2640
OY	2784	AACAATTTGCTTAACAAATGGGCTCTTTAAAAAGATTACCCCTTATATGACTACCAAGCCATG	2843
Db	2641	AACAATTTGCTTAACAAATGGGCTCTTTAAAAAGATTACCCCTTATATGACTACCAAGCCATG	2700
OY	2844	TGTAGAAGCCAAACAAGAAAGACAGCATGGGCCCCATGAGCTCCTTGATCCTTATATGCC	2903
Db	2701	TGTAGAAGCCAAACAAGAAAGACAGCATGGGCCCCATGAGCTCCTTGATCCTTATATAGCC	2760
OY	2904	TTTCCTCTCTGACAGTAAATATGATCATGACAGAACTGTCTTGTTCGTGGTGAATTTAAC	2963
Db	2761	TTTCCTCTCTGACAGTAAATATGATCATGACAGAACTGTCTTGTTCGTGGTGAATTTAAC	2820
OY	2964	CTCTGAGTGGTGGCGACTCCGATATGACAGCTTAAAGCCAGAAATTTAAACAGACCCTG	3023
Db	2821	CTCTGAGTGGTGGCGACTCCGATATGACAGCTTAAAGCCAGAAATTTAAACAGACCCTG	2880
OY	3024	GAGCCTTGTGATCTGTAATATCCAGATTCGTCTGAGGCGACATCAAGAGACTACA	3083
Db	2881	GAGCCTTGTGATCTGTAATATCCAGATTCGTCTGAGGCGACATCAAGAGACTACA	2940
OY	3084	GGGAATATTGCTTTGTGAAGACTGCTCCAAGTCCCTTTGTCTCCAGCAAAATCCCAAGCAGC	3143
Db	2941	GGGAATATTGCTTTGTGAAGACTGCTCCAAGTCCCTTTGTCTCCAGCAAAATCCCAAGCAGC	3000
OY	3144	AACCTGTTCATGGTGGTGGTGGAGCAGCAGCTGCTCTGTGAATCTGTGGCCCCCATCACC	3203
Db	3001	AACCTGTTCATGGTGGTGGTGGAGCAGCAGCTGCTCTGTGAATCTGTGGCCCCCATCACC	3060
OY	3204	ATGGCACCATTGAATTCAGGTATATGATCCCTTAAGTGAAGCTGCTAAAG	3257
Db	3061	ATGGCACCATTGAATTCAGGTATATGATCCCTTAAGTGAAGCTGCTAAAG	3114
RESULT 10			
AAS01407			
ID	AAS01407 standard; cDNA; 3057 BP.		
XX	AAS01407:		
AC			
XX	04-JUL-2001 (first entry)		
DT			
XX			
DE	Human secreted soluble alpha2delta calcium channel subunit #4 cDNA.		
XX			
KW	Human: secreted calcium channel alpha2delta subunit; alpha2delta-2;		
KW	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;		
KW	gabapentin; scintillation proximity assay; SPA; nickel flashplate assay		
KW	filter binding assay; wheat germ lectin flashplate assay; ss.		
XX			
OS	Homo sapiens.		
XX			
EH	Key		
FT	1..3057		
FT	/*tag- a		
FT	/partial		
FT	/product- "Alpha2delta calcium channel subunit #4"		
FT	/note- "this sequence lacks a stop codon"		
XX	MO200119870-A2.		
FN			
XD	22-MAR-2001		

XX	PF	18-SEP-2000; 2000MO-EP09137.
XX	PR	16-SEP-1999; 99US-0397550.
XX	PA	(WARN) WARNER LAMBERT CO.
PI	Brown JP, Bertelli F;	
XX	MP1; 2001-235262/24.	
DR	P-PsDB; AAU01017.	
XX	Calcium channel alpha2delta subunits, useful in e.g. SPA assays,	
PT	Fluorescence assays, Nickel Flashplate assays, Filter binding assays or	
XX	Wheat Germ Lectin Flashplate assays -	
PS	Claim 39; Page 69-70; 160pp; English.	
XX	The present sequence encodes for human secreted calcium channel	
CC	alpha2delta subunit #4 which is soluble and retains the functional	
CC	characteristics of the full length or wild type alpha2delta subunit	
CC	(AAU01025) from which it is derived. The invention relates to truncated	
CC	alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins	
CC	which retain their affinity for radioactively labeled gabapentin. The	
CC	alpha2delta subunit is 1 of the components of the heteromultimeric	
CC	voltage-dependent calcium channel (VDC) complexes present in neuronal	
CC	and non-neuronal tissues including heart and skeletal muscle. Numerous	
CC	soluble forms of the human calcium channel alpha2delta subunits	
CC	(AAU01014-AAU01024 and AAU01033-AAU01038) and 5 soluble forms of the	
CC	porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are	
CC	described. The secreted soluble alpha2delta subunit may be used in assays	
CC	e.g. schnittillation proximity assay (SPA), flashplate, nickel flashplate,	
CC	filter binding or wheat germ lectin flashplate assays to detect or	
CC	measure the binding or interaction of a ligand (e.g. gabapentin,	
CC	L-Norepinephrine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,	
CC	L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel	
CC	alpha2delta subunit.	
SQ	Sequence 3057 BP; 848 A; 692 C; 778 G; 738 T; 1 other:	
Query Match	81.1%; Score 3056.6; DB 22; Length 3057;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 3057; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	144 ATGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGCTTCGCTGCC 203	
DB	1 ATGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGCTTCGCTGCC 60	
OY	204 GCGCTTCTTACGCGCGCGGTGGGGAGCTGTGCCTCGAGCAGATNACCCTTCC 263	
DB	61 GCGCTTCTTACGCGCGCGGTGGGGAGCTGTGCCTCGAGCAGATNACCCTTCC 120	
OY	264 GTGGTGCAACTCTGGGECCTGGGCTTTTGGTGGGGAGATTAATCCATTGCTGAATAC 323	
DB	121 GTGGTGCAACTCTGGGECCTGGGCTTTTGGTGGGGAGATTAATCCATTGCTGAATAC 180	
OY	324 TCCGGTCCCACTTCTGCAAAAAGAATAACAAGATNTGAGAAGAGTTGCCATTAGAA 383	
DB	181 TCCGGTCCCACTTCTGCAAAAAGAATAACAAGATNTGAGAAGAGTTGCCATTAGAA 240	
OY	384 GAAATTTGATGGCCTCAACTGTGTAAAGAAGCTGCGAAGAACATGAGAGATGTTTAC 443	
DB	241 GAAATTTGATGGCCTCAACTGTGTAAAGAAGCTGCGAAGAACATGAGAGATGTTTAC 300	
OY	444 AAGAACTCTGAGGCGGTGAGGCGTCTGTGTGAGGCTGAGAGGCTGAGAGAACATCAACAT 503	
DB	301 AAGAACTCTGAGGCGGTGAGGCGTCTGTGTGAGGCTGAGAGAACATCAACAT 360	
OY	504 GAATTTGATGCAAGATTTGAGATGAATCAATCAATGCTGTGCTGATTAATGAAGAGAC 563	
DB	361 GAATTTGATGCAAGATTTGAGATGAATCAATCAATGCTGTGCTGATTAATGAAGAGAC 420	
OY	564 AAGAGCGGGAATTTTTTGAGACTGGGAAAGAATTCATCTTAGCCCCAAATGACCATTTT 623	



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Db 421 AAGAGCGGGAATTTTGGCTGGGAAAGAAATTCATCTTACCCCAATGACCATTTT 480  
QY 624 AATAATTTGCTGTGAACATCAGTCTAAGTACGTCCCACTACCACGACATGTACAC 683  
|||||  
Db 481 AATAATTTGCTGTGAACATCAGTCTAAGTACGTCCCACTACCACGACATGTACAC 540  
QY 684 AAGACCCTGCAATTTGTCAATGGGGTTTATTTGGTCAATCTCTAAACAAGTTTGTGA 743  
541 AAGACCCTGCAATTTGTCAATGGGGTTTATTTGGTCAATCTCTAAACAAGTTTGTGA 600  
QY 744 GATTAATTTGACCGGTGACCCATCTCTCATATGGCAGTACTTTGGAAATGCAAGGCTTT 803  
601 GATTAATTTGACCGGTGACCCATCTCTCATATGGCAGTACTTTGGAAATGCAAGGCTTT 660  
QY 804 TTTAGCAGTATCCGGGGATTTAAATGGGAAACAGATGAGAAATGATCAATGGCTTCGAC 863  
661 TTTAGCAGTATCCGGGGATTTAAATGGGAAACAGATGAGAAATGATCAATGGCTTCGAC 720  
QY 864 TCCAGAACCCGAAATGATGATCCAGGACGCAACTTCCGAAAGAGTGTCTATTTTA 923  
721 TCCAGAACCCGAAATGATGATCCAGGACGCAACTTCCGAAAGAGTGTCTATTTTA 780  
QY 924 GTTGACGTACAGTGGCAGCATGAAAGACTCCGTCTGACTATGCGGAAAGCACTCTCA 983  
781 GTTGACGTACAGTGGCAGCATGAAAGACTCCGTCTGACTATGCGGAAAGCACTCTCA 840  
QY 984 TCCATTTTGGATACACATTTGGGGATGATGACTCTTCAACATATTTGCTTTATATGAGGAG 1043  
841 TCCATTTTGGATACACATTTGGGGATGATGACTCTTCAACATATTTGCTTTATATGAGGAG 900  
QY 1044 CTTCACATGTGGAACCTTGCTGATGGAACCTTTGGTGAACCCGACAGCAACAA 1103  
901 CTTCACATGTGGAACCTTGCTGATGGAACCTTTGGTGAACCCGACAGCAACAA 960  
QY 1104 GAGCACTTCAGGAGACATCTGGACAACTTTTCCCAAGAAATGGAATGTTGATATATA 1163  
961 GAGCACTTCAGGAGACATCTGGACAACTTTTCCCAAGAAATGGAATGTTGATATATA 1020  
QY 1164 GCTCGATGAGAGCCTTCAACATCTGAGTGAATTTCAACCCACAGGGGACAAAGATATC 1223  
1021 GCTCGATGAGAGCCTTCAACATCTGAGTGAATTTCAACCCACAGGGGACAAAGATATC 1080  
QY 1224 TGCAGTACGCCATCATGCTCATTAAGTGGGGGTGAGACACTATGATATCAATCTTT 1283  
1081 TGCAGTACGCCATCATGCTCATTAAGTGGGGGTGAGACACTATGATATCAATCTTT 1140  
QY 1284 GCAAAATTCATTTGGCCAGATCGAAAGTTCGATCTTCACATACCTTATGAGAGAG 1343  
1141 GCAAAATTCATTTGGCCAGATCGAAAGTTCGATCTTCACATACCTTATGAGAGAG 1200  
QY 1344 GCTCGATTTGAGACAAATCTAAAGTGGAGTGGCCGTGGCAACAAAGATTTTTTACCAG 1403  
1201 GCTCGATTTGAGACAAATCTAAAGTGGAGTGGCCGTGGCAACAAAGATTTTTTACCAG 1260  
QY 1404 ATCTCCACTTTGGCTGATGTGACAGAGATGTCAATGAAATCTTCAAGCTTATGACCGG 1463  
1261 ATCTCCACTTTGGCTGATGTGACAGAGATGTCAATGAAATCTTCAAGCTTATGACCGG 1320  
QY 1464 CCCAAATTCATCGACAGAGACATGATGTGTGACCCGAAGCTTCAATGACAGCACT 1523  
1321 CCCAAATTCATCGACAGAGACATGATGTGTGACCCGAAGCTTCAATGACAGCACT 1380  
QY 1524 CTGACTGATATCAGGAGCCCGCTGATGACCACTGTAGCAATGACCTGTGTTATGATAG 1583  
1381 CTGACTGATATCAGGAGCCCGCTGATGACCACTGTAGCAATGACCTGTGTTATGATAG 1440  
QY 1584 CAGACGAAACCAAGATGGAAGGCAATCTTCTGGAGTGGTTGGCAGACGATGTCACAGTG 1643  
1441 CAGACGAAACCAAGATGGAAGGCAATCTTCTGGAGTGGTTGGCAGACGATGTCACAGTG 1500  
QY 1644 AAGAACTTGTGAAGCAATCCCAATACAAATGAGGATTCACGGTTATGACCTTTGCA 1703  
|||||

Db 1501 AAGAACTTCGAAGACCATCCCAATACAAATGATGAGGATTCACGGTTATGCCTTTGCA 1560  
QY 1704 ATCACAAAATTAATGGATATATCTGACGCATCCGGAATCAGGCTGTGATGAGAAGGA 1763  
Db 1561 ATCACAAAATTAATGGATATATCTGACGCATCCGGAATCAGGCTGTGATGAGAAGGA 1620  
QY 1764 AAAAAGCGAAGAACTTAATAGTACGCTTCTCTGAGTGGAGTGGAGAAC 1823  
1621 AAAAAGCGAAGAACTTAATAGTACGCTTCTCTGAGTGGAGTGGAGAAC 1680  
QY 1824 CGAGATGACGTGTTGAGAAATGCTATGTAATCGAAAGCGGGGAAGTTTCCATGAG 1883  
1681 CGAGATGACGTGTTGAGAAATGCTATGTAATCGAAAGCGGGGAAGTTTCCATGAG 1740  
QY 1884 GTGAAGAAGCACTGAGCAAAAGGAAACGGGTTTGGTGAATGCAAAATGACTATTAAT 1943  
1741 GTGAAGAAGCACTGAGCAAAAGGAAACGGGTTTGGTGAATGCAAAATGACTATTAAT 1800  
QY 1944 ACAGACATCAAGGTAATCTCTTCACTTTAGTGTGGCGCTTTCAGAGTCAATGGAAA 2003  
1801 ACAGACATCAAGGTAATCTCTTCACTTTAGTGTGGCGCTTTCAGAGTCAATGGAAA 1860  
QY 2004 TATTTCTCCGAGGAATGTAACCATCGAAGAGCGCTGATGACTTTAGAACATCCCGAT 2063  
1861 TATTTCTCCGAGGAATGTAACCATCGAAGAGCGCTGATGACTTTAGAACATCCCGAT 1920  
QY 2064 GTGTCTTGGCAGATGAATGTCTCTACTGCAACACTGACCTACACCCCTGACGCCCAT 2123  
1921 GTGTCTTGGCAGATGAATGTCTCTACTGCAACACTGACCTACACCCCTGACGCCCAT 1980  
QY 2124 CTTCTCACTTTGAAGCCGTTAAGCTCTCACTTAAAGGCAAGAACCTCTGCTCCAGTGT 2183  
1981 CTTCTCACTTTGAAGCCGTTAAGCTCTCACTTAAAGGCAAGAACCTCTGCTCCAGTGT 2040  
QY 2184 GATTAAGAAATTAATCCAAAGACCTTTTGAAGCGGGGTGATGAGCCCAATTAAGGG 2243  
2041 GATTAAGAAATTAATCCAAAGACCTTTTGAAGCGGGGTGATGAGCCCAATTAAGGG 2100  
QY 2244 TATTTGACCAAGCCTGGCCCTCAACAAATCTGAAAAATTCGACAAAGGCGCTGAGGTGCG 2303  
2101 TATTTGACCAAGCCTGGCCCTCAACAAATCTGAAAAATTCGACAAAGGCGCTGAGGTGCG 2160  
QY 2304 TTTCCGCGGACTGCGACGCGGCTCTCCAGATCAACCTGTTTGTGCGGGCTGAGCAGCTC 2363  
2161 TTTCCGCGGACTGCGACGCGGCTCTCCAGATCAACCTGTTTGTGCGGGCTGAGCAGCTC 2220  
QY 2364 ACCAATCAAGACTTCTCTGAAAGCTGGGCAAGAGAACATTTTAAAGCAGACCATTTTC 2423  
2221 ACCAATCAAGACTTCTCTGAAAGCTGGGCAAGAGAACATTTTAAAGCAGACCATTTTC 2280  
QY 2424 CCTCTCTGGTACCGAAGACCGGCTGAGCAGATTCAGGAGACTTCTGCTACATGATCCCA 2483  
2281 CCTCTCTGGTACCGAAGACCGGCTGAGCAGATTCAGGAGACTTCTGCTACATGATCCCA 2340  
QY 2484 TTTGAGCATGAGACCACTGAATTAAGCAATGTGTGACAGCAAGTACATCCAGCTC 2543  
2341 TTTGAGCATGAGACCACTGAATTAAGCAATGTGTGACAGCAAGTACATCCAGCTC 2400  
QY 2544 CTGATGAAAGGAAATCTCCGTGTGGTGGCAGCTGTAGGCATTTCAAGTAACTGAAATTT 2603  
2401 CTGATGAAAGGAAATCTCCGTGTGGTGGCAGCTGTAGGCATTTCAAGTAACTGAAATTT 2460  
QY 2604 TTTCCAAAGGAAGTTCTGTGACTGCCAGCAGACAGAGTGTCTTCCGTGATGGAATGCTCC 2663  
2461 TTTCCAAAGGAAGTTCTGTGACTGCCAGCAGACAGAGTGTCTTCCGTGATGGAATGCTCC 2520  
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2581 GTGTCTGAAGACTACACAGACTGAGACTTTTGTGTGAGATCGAGGAGCTGTATG 2640  
|||||



QY	984	TCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAAATTCCTTATTAATGAGAG	1043
Db	841	TCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATTAATTCCTTATTAATGAGAG	900
QY	1044	CTTACATATGGAACCTTGGCTGTAATGGAACCTTTGGTGCACAGCCGACAGACAAACAA	1103
Db	901	CTTACATATGGAACCTTGGCTGTAATGGAACCTTTGGTGCACAGCCGACAGACAAACAA	960
QY	1104	GAGCACTTCAGGGAGCATCTGAGCAAACTTTGCCCAAGGAATTTGGAATGTTGGATATA	1163
Db	961	GAGCACTTCAGGGAGCATCTGAGCAAACTTTGCCCAAGGAATTTGGAATGTTGGATATA	1020
QY	1164	GCTCTGATGATAGCCCTTCAACATTTCTGATGATTTCAACACACAGGACAAAGAAATATC	1223
Db	1021	GCTCTGATGATAGCCCTTCAACATTTCTGATGATTTCAACACACAGGACAAAGAAATATC	1080
QY	1224	TGCGATGAGCCATCATGCTCATTAACATGATGAGGGGGGTGGACACTTATCATATCTTT	1283
Db	1081	TGCGATGAGCCATCATGCTCATTAACATGATGAGGGGGGTGGACACTTATCATATCTTT	1140
QY	1284	GCAAAATACAAATTTGGCCAGATCGAAAGGTTCCGATCTTCACATATACCTCATTTGGACGAG	1343
Db	1141	GCAAAATACAAATTTGGCCAGATCGAAAGGTTCCGATCTTCACATATACCTCATTTGGACGAG	1200
QY	1344	GCTGCGTTTGCACACAACTTAAAGTGATGGCCTGTGCCAAACAAAGATTTTTTACCAG	1403
Db	1201	GCTGCGTTTGCACACAACTTAAAGTGATGGCCTGTGCCAAACAAAGATTTTTTACCAG	1260
QY	1404	ATCTCACCTTGGCTCATATGTCAGAGGAATGATGATGATACCTTACCTTGCTTACGCGG	1463
Db	1261	ATCTCACCTTGGCTCATATGTCAGAGGAATGATGATGATGATACCTTACCTTGCTTACGCGG	1320
QY	1464	CCCAAGTCATCCAGCAGGAGCATGATGTTGGTGTGGACCGAACCTTACATTTGACACACT	1523
Db	1321	CCCAAGTCATCCAGCAGGAGCATGATGTTGGTGTGGACCGAACCTTACATTTGACACACT	1380
QY	1524	CTGACTGATGATCAGGGCCCGCTCTGATGACCACTGATAGCCATGCTGTGTTAGTAAG	1583
Db	1381	CTGACTGATGATCAGGGCCCGCTCTGATGACCACTGATAGCCATGCTGTGTTAGTAAG	1440
QY	1584	CAGAACGAAACCAAGTCGAAGGGCATTTCTTGGAGTGGTGGACACATGTCGCCAGTG	1643
Db	1441	CAGAACGAAACCAAGTCGAAGGGCATTTCTTGGAGTGGTGGACACATGTCGCCAGTG	1500
QY	1644	AAAGAACTTCTGAAAGACATATCCCAATACAAAGTTAGGATTCAGGGTATGCTTTTGA	1703
Db	1501	AAAGAACTTCTGAAAGACATATCCCAATACAAAGTTAGGATTCAGGGTATGCTTTTGA	1560
QY	1704	ATCACAAATTAATGRTATATCTTGACGATCCGAACTCAGGCTCGGTATCGAAGCAAGA	1763
Db	1561	ATCACAAATTAATGRTATATCTTGACGATCCGAACTCAGGCTCGGTATCGAAGCAAGA	1620
QY	1764	AAAAAGCGAAGGAACCTTACTATATAGTAGCGTTGACCTCTCTGAGGTGAGTGGGAAGAC	1823
Db	1621	AAAAAGCGAAGGAACCTTACTATATAGTAGCGTTGACCTCTCTGAGGTGAGTGGGAAGAC	1680
QY	1824	CGAGATGACGTTTAGAAATGCTATGATGATGAAAGACGSGGAAGTTTCCATGAG	1883
Db	1681	CGAGATGACGTTTAGAAATGCTATGATGATGAAAGACGSGGAAGTTTCCATGAG	1740
QY	1884	GTGAAGAAGACAGTGGACAAAGGGAAGCGGTTTGTGATATACAAATGACTACTATTAT	1943
Db	1741	GTGAAGAAGACAGTGGACAAAGGGAAGCGGTTTGTGATATACAAATGACTACTATTAT	1800
QY	1944	ACAGACATTCAGGGTACTTCCTTCACTTAAAGTTAGGTGTGGCGCTTTTCCAGAGGTTCAGGAAA	2003
Db	1801	ACAGACATTCAGGGTACTTCCTTCACTTAAAGTTAGGTGTGGCGCTTTTCCAGAGGTTCAGGAAA	1860
QY	2004	TATTTCTTCGAGGAATGTAAACATTCGAAGAAGCCGTGCATGACTTGAACATCCGAT	2063
Db	1861	TATTTCTTCGAGGAATGTAAACATTCGAAGAAGCCGTGCATGACTTGAACATCCGAT	1920

QY	2054	GTGTCTTGGCAGATGAATGGTCTCTACTGCAACACTGACCTTACACCTTGAGACCCGCAT	2123
Db	1921	GTGTCTTGGCAGAAATGGTCTACTGCAAACTGTGACCTACACCTTGAGACCCGCAT	1980
QY	2124	CTGTCTCAGTTAGAAAGCATTAAGTCTACCTAAAGGCAAAAGAACTGTGTCCAGT	2183
Db	1981	CTGTCTCAGTTAGAAAGCATTAAGTCTACCTAAAGGCAAAAGAACTGTGTCCAGT	2040
QY	2184	GATTAAGAATTTGATCCAAAGAGTCTTTTGTACGGGGTGTGAGTGGCCCATTTGAACG	2243
Db	2041	GATTAAGAATTTGATCCAAAGAGTCTTTTGTACGGGGTGTGAGTGGCCCATTTGAACG	2100
QY	2244	TATTGGACAGCCTTGCGCCCTCAACAATCTGAAAAATCTGCAAGGGCGTGGAGTTGCC	2303
Db	2101	TATTGGACAGCCTTGCGCCCTCAACAATCTGAAAAATCTGCAAGGGCGTGGAGTTGCC	2160
QY	2304	TTTCTCGGCACTGCGAGGGGCTCTCCAGATTCAACTGTTGTGTGCGGGGCTGACAGCTC	2353
Db	2161	TTTCTCGGCACTGCGAGGGGCTCTCCAGATTCAACTGTTGTGTGCGGGGCTGACAGCTC	2220
QY	2354	ACCATTCAGAGACTTCTGAAAAGCTGGGCGACAAAGAGAACTTTTAAAGCGAGACATTTCC	2423
Db	2221	ACCATTCAGAGACTTCTGAAAAGCTGGGCGACAAAGAGAACTTTTAAAGCGAGACATTTCC	2280
QY	2424	CTCTCTGTGTCAGGAAGACCGCTGAGCAGATTCACAGGAGCTTCTGTCTACTCGATCCCA	2483
Db	2281	CTCTCTGTGTCAGGAAGACCGCTGAGCAGATTCACAGGAGCTTCTGTCTACTCGATCCCA	2340
QY	2484	TTTCAGACTGGACAGTCAATTAAGAAATGTGTGACAGCACTACATCCATCCAGCTC	2543
Db	2341	TTTCAGACTGGACAGTCAATTAAGAAATGTGTGACAGCACTACATCCATCCAGCTC	2400
QY	2544	CTGGATCAAGGGAATCTCTGTGTGTGGCGAGCTTAGCAATTCAGATGAAGAACTTGAAATTT	2603
Db	2401	CTGGATCAAGGGAATCTCTGTGTGTGGCGAGCTTAGCAATTCAGATGAAGAACTTGAAATTT	2460
QY	2604	TTCCAAAGGAAGTTCTGTGAGCTGCCAGCAGACAGTGTGCTTCCCTGGATGTGGCAATGCTCC	2663
Db	2461	TTCCAAAGGAAGTTCTGTGAGCTGCCAGCAGACAGTGTGCTTCCCTGGATGTGGCAATGCTCC	2520
QY	2664	ATTCAGCTGTATATGAGACTGTGGAATTTGTACCTCATAGACAAATTAATGATTTAATTTG	2723
Db	2521	ATTCAGCTGTATATGAGACTGTGGAATTTGTACCTCATAGACAAATTAATGATTTAATTTG	2580
QY	2724	GTGTCTGAAGACTACACACAGACTGGGAGATTTTTGTGTGTAGATTCAGGGAGAGCTGTGATG	2783
Db	2581	GTGTCTGAAGACTACACACAGACTGGGAGATTTTTGTGTGTAGATTCAGGGAGAGCTGTGATG	2640
QY	2784	AACAATTTGCTAACAATTTGGGCTCTTTTAAAGAAATTAACCTTTATGACTACCAAGCATG	2843
Db	2641	AACAATTTGCTAACAATTTGGGCTCTTTTAAAGAAATTAACCTTTATGACTACCAAGCATG	2700
QY	2844	TGTAGAGCCACAAGAAAGCAAGCATGGCGGCCATGGCCTCTGTGATCCTTAAATGCC	2903
Db	2701	TGTAGAGCCACAAGAAAGCAAGCATGGCGGCCATGGCCTCTGTGATCCTTAAATGCC	2760
QY	2904	TTTCCCTGTGCAAGTAAATTAAGATCAAGACAGAACTTGTCTTGTCTGTGGGAATTTAAC	2963
Db	2761	TTTCCCTGTGCAAGTAAATTAAGATCAAGACAGAACTTGTCTTGTCTGTGGGAATTTAAC	2820
QY	2964	CTTCTGAGTTGGTGCGACTGCCATATGACAGCTTAAAGCCACAGAAATTTGAAGACGACCTGG	3023
Db	2821	CTTCTGAGTTGGTGCGACTGCCATATGACAGCTTAAAGCCACAGAAATTTGAAGACGACCTGG	2880
QY	3024	GAGCCTTGTGATCTGAATATATCCAGACTTTCGTCTGTGAGCGGACCATCTCAAGGAGACTACA	3083
Db	2881	GAGCCTTGTGATCTGAATATATCCAGACTTTCGTCTGTGAGCGGACCATCTCAAGGAGACTACA	2940
QY	3084	GGGAATTTATGCTGTGGAAGACATGCTCCAAAGTCTTTGTCTATCCACCAAAATTCCTCAAGCAGC	3143
Db	2941	GGGAATTTATGCTGTGGAAGACATGCTCCAAAGTCTTTGTCTATCCACCAAAATTCCTCAAGCAGC	3000
QY	3144	AACCTGTCATGATGTGTGTGAGCAGCACTGCTCTGTGAATCTGTGGGCCCCCATTC	3200

Db 3001 AACCTGTCATGTCGTGTGTGAGACAGAGCTGCTCTGTGATCTGTGGCCCCATC 3057

## RESULT 12

AAA09260  
ID AAA09260 standard; cDNA: 2008 BP.

AC AAA09260:

AT 10-AUG-2000 (first entry)

DE Human alpha-2-delta-C gene 3' splice variant.

KM alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cyostatic;

KW anticonvulsant; antitrigemine; antiparkinsonian; antidepressant;

XX splice variant; 98.

OS Homo sapiens.

PN MO200020450-A2.

PD 13-APR-2000.

PF 07-OCT-1999; 99MO-US23519.

PR 07-OCT-1998; 98US-0103322.

PR 30-OCT-1998; 98US-0106473.

PR 29-DEC-1998; 98US-0114088.

XX (WARN ) WARNER LAMBERT CO.

PI Johns MA, Moldover B, Olford JD;

DR MPI: 2000-303744/26.

XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D

PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,

XX anxiety, multiple sclerosis or cancer

PS Claim 22: Page 84-85; 88pp; English.

XX The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.

CC The gene has been mapped to chromosome 3p21.1. This gene and the related

CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells

CC from abnormal calcium flux by introducing expression vectors containing

CC the respective gene into mammalian cells. The antisense genes are also

CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein

CC is a high-affinity binding target of the anti-convulsant drug gabapentin.

CC Therefore, alpha-delta-2 proteins may also be targeted to treat

CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic

CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),

CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or

CC addiction syndromes, mood, depression or cancer.

XX Sequence 2008 BP: 555 A; 454 C; 536 G; 462 T; 1 other:

Query Match 50.6%; Score 1908.2; DB 21; Length 2008;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1910; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TACTATAGGCGCGCCGCAATTCGACAGAGGCGCGGAGGAGCAAGCCCGC 60  
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DB 61 GCGCTGCGCCACCGCGCTCGCGGAGCTCCCGGCGCTCTCTGCGCCCGCAGC 120  
QY 121 GGGGCGGTGGGAGGAGCCAGCATGCGCGGCGCGGCGCTGCGCGCGCTCCGGG 180  
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QY 181 GGGCGTGGCGCGCTTCTGCGTCCCGCGCTTCTCTAGCGCGCGCTGGGAGAGTGGTCCCT 240  
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QY 661 AAGTACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
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DB 1021 ACATTAATGCTTAATGAGAGCTTCACTAGTGAAGCTTCACTAGTGAAGCTTCACT 1080  
QY 1081 TGCAGCGCAG 1140  
DB 1081 TGCAGCGCAG 1140  
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DB 1141 AAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
QY 1201 ACCACAGGAG 1260  
DB 1201 ACCACAGGAG 1260  
QY 1261 TGGACACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320

Accession	Gene	Protein	Species	Length (aa)	CDNA	CDNA Length (bp)	CDNA Description
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D8	1321	TCACATATCCCATTTGGACGAGAGCGCTTGGCTTTGCGACACAACTTAAAGTGGATGGCTGTG	1380				
QY	1381	CCAACAAAGATTTTTTACCAGCATCTCCACCTTGGCTGATGTGGAGAGAAATGTCATGG	1440				
D8	1381	CCAACAAAGATTTTTTACCAGCATCTCCACCTTGGCTGATGTGGAGAGAAATGTCATGG	1440				
QY	1441	AATATCTTACAGTGTGTAGCCGCGCCCAAAAGTCATGACACAGAGCATGATGTGGTGA	1500				
D8	1441	AATATCTTACAGTGTGTAGCCGCGCCCAAAAGTCATGACACAGAGCATGATGTGGTGA	1500				
QY	1501	CCGAACCTTACATTTGACACACTCTGACATGATGATCAGAGGCGCCGTCTGATGACACTG	1560				
D8	1501	CCGAACCTTACATTTGACACACTCTGACATGATGATCAGAGGCGCCGTCTGATGACACTG	1560				
QY	1561	TACCATATGCTGTGTGTAGTAAAGCAAGAACGATTCGAAAGGCACTTTTGGGAG	1620				
D8	1561	TACCATATGCTGTGTGTAGTAAAGCAAGAACGATTCGAAAGGCACTTTTGGGAG	1620				
QY	1621	TGGTGGGCAACATATGTCGACGAGAAAGACTTCTGAGAACCATCCCAATACAGTTAG	1680				
D8	1621	TGGTGGGCAACATATGTCGACGAGAAAGACTTCTGAGAACCATCCCAATACAGTTAG	1680				
QY	1681	GGATTCACCGTATATCCTTTGGCAATCACAAATTAATGGTATATCTTACATCCATCCGGAAC	1740				
D8	1681	GGATTCACCGTATATCCTTTGGCAATCACAAATTAATGGTATATCTTACATCCATCCGGAAC	1740				
QY	1741	TCAGCTGTGTAGCAAGAGAGAAAAAGCGAAGAAACCTTAATATAGTAGGTTGACC	1800				
D8	1741	TCAGCTGTGTAGCAAGAGAGAAAAAGCGAAGAAACCTTAATATAGTAGGTTGACC	1800				
QY	1801	TCCTTGAGGTGAGAGGGAAGACCGAGATGACGCTTGGAGAAATGCTATAGTGAATCGAA	1860				
D8	1801	TCCTTGAGGTGAGAGGGAAGACCGAGATGACGCTTGGAGAAATGCTATAGTGAATCGAA	1860				
QY	1861	AGACGGGGAAGTTTCCATGAGAGTGAAGAAGACAGTGGCAAAAGGGAACGGGTTT	1917				
D8	1861	AGACGGGGAAGTTTCCATGAGAGTGAAGAAGACAGTGGCAAAAGGGAACGGGTTT	1917				
RESULT 13							
AA251626							
XX	AA251626	standard; cDNA; 1774 BP.					
AC	AA251626;						
XX							
DT	21-JUN-2000	(first entry)					
XX							
DE	Human membrane channel protein-10 (MECHP-10) cDNA.						
XX							
KW	Membrane channel protein-10; MECHP-10; diagnosis; treatment; lymphoma;						
KW	cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;						
KW	inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;						
KW	diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;						
KW	muscular disorder; myocarditis; Duchenne's muscular dystrophy; noctropic						
KW	cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiac;						
KW	neurological disorder; Alzheimer's disease; Parkinson's disease; human;						
KW	Huntington's disease; antiarteriosclerotic; hepatotropic; cyostatic;						
KW	anti-HIV; antianemic; neuroprotective; immunomodulatory; antidiabetic;						
KW	hypotensive; vasotropic; antisthmatic; antinflammatory; antidepressant;						
KW	anticonvulsant; thrombolytic; antiparkinsonian; immunostimulant; ss.						
XX							
OS	Homo sapiens.						
XX							
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FT	misc_binding	/product= "MECHP-10"					
FT		1275..1322					

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FT      /tag= b
FT      /bound_molety="Probe or Primer"
XX      WO200012711-A2.
XX      09-MAR-2000.
XX      02-SEP-1999; 99WO-US20468.
XX      02-SEP-1998; 98US-0145815.
XX      12-NOV-1998; 98US-0191283.
XX      09-DEC-1998; 98US-0208821.
XX      26-JAN-1999; 99US-0237506.
XX      10-FEB-1999; 99US-0247891.
XX      (INCY-) INCYTE PHARM INC.
XX      Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yue H;
XX      Lal P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzai Y;
XX      WPI; 2000-256643/22.
XX      P-PSDB; AAY70460.
XX      Novel human membrane channel protein and polynucleotide useful for
XX      diagnosing and treating cell proliferative, inflammatory, secretory,
XX      osmoregulatory, muscular, cardiovascular and neurological disorders
XX      Claim 9; Page 124-125; 140pp; English.
XX
XX      The present sequence is a cDNA identified in Incyte clone 3148427
XX      derived from ADBRONO4 cDNA library. It encodes human membrane channel
XX      protein-10 (MECHP-10), which is expressed in cardiovascular, endocrine
XX      and nervous tissues. Anti-MECHP antibodies can be used as therapeutic
XX      antagonists and reagents for diagnosis and monitoring diseases. MECHP
XX      cDNA can be used for diagnosis of MECHP-related diseases and gene
XX      mapping. MECHP can be used for treatment of cell proliferative disorders
XX      such as bursitis and atherosclerosis, cancers like lymphoma and sarcoma,
XX      inflammatory disorders like AIDS and Addison's disease, transport or
XX      secretory disorders like cystic fibrosis and diabetes mellitus,
XX      osmoregulatory disorders like diarrhoea and renal failure, muscular
XX      disorders like myocardiitis and Duchenne's muscular dystrophy,
XX      cardiovascular disorders like hypertension and vasculitis, congenital
XX      lung anomalies like bronchitis and asthma and neurological disorders like
XX      Alzheimer's disease, Parkinson's disease and Huntington's disease.
XX
XX      Sequence 1774 BP; 539 A; 366 C; 440 G; 429 T; 0 other:
XX
XX      Query Match 41.0%; Score 1545; DB 21; Length 1774;
XX      Best Local Similarity 95.8%; Pred. No. 0;
XX      Matches 1614; Conservative 1; Mismatches 51; Indels 19; Gaps 2
XX
XX      252 ATACGCGCTTCGCTGGTGAAGCTCTGGGCGCTGGGCTTTGGTGGGAGATAAATCATTT 311
XX      ||||| || || || || || || || || || || || || || || || || || || ||
XX      8 ATACCGTCGACCCCGCGTCTCTGTGAAGGAACCTCGGGCTGCTTGGGGAGAAAAAATC 67
XX
XX      312 GCTGCTAACTACCTCCGTTCCAGCTTTCGCAAAAGAAATACAAAGATGAGAAAGAC 371
XX      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX      68 CATGGCGTAATACCTGGGTTCCAGGCTTCGCAAAAGAAATACAAAGATGAGAAAGAC 127
XX
XX      372 GTTGGCATGAAGAA-ATTGATGGCTCCACTGCTGTAAGAAAGCTGGCAAGAACATGGA 430
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XX
XX      491 ACACCTGAACATGAATTTGATGACAGACTTACAGATGAATATCTCAATGCTGCTGAT 550
XX      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX      248 ACACCTGAACATGAATTTGATGACAGACTTACAGATGAATATCTCAATGCTGCTGAT 307
XX      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX      551 AATGAAGAAGGACAAAGCGGAATTTTTTGAGCTGGGAAAGAAATTCATTGATGATG 610
XX      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 308 AAATGAAGGACAAAGCGGAATTTTGGACCTGGGAAGGATTCATCTTAGCCCC 367  
 QY 611 AAATGACCATTTAAATTAATTTGGCTGTGAACATCAGTCTAAGTACGTCCAAAGTACCAC 670  
 Db 368 AAATGACCATTTAAATTAATTTGGCTGTGAACATCAGTCTAAGTACGTCCAAAGTACCAC 427  
 QY 671 GAACATGTACAAAGAACCCCTGCAATGTCTCAATGGGTTTATGTGCTCAATCTCTAAA 730  
 Db 428 GAACATGTACAAAGAACCCCTGCAATGTCTCAATGGGTTTATGTGCTCAATCTCTAAA 487  
 QY 731 CAAGTTTTGTAGATTAACCTTTGACCGTGAACCCATCTCTCATATATGACAGTACTTTGGAAG 790  
 Db 488 CAAGTTTTGTAGATTAACCTTTGACCGTGAACCCATCTCTCATATATGACAGTACTTTGGAAG 547  
 QY 791 TGGAAAGGGGTTTTTATGAGGAGTATCCGGGGATTAATTTGGAACCAATAGATGAGT 850  
 Db 548 TGGAAAGGGGTTTTTATGAGGAGTATCCGGGGATTAATTTGGAACCAATAGATGAGT 607  
 QY 851 CATTTGCCCTTGACCTGAGAACCGAAATGTTACATCCAGGACCAACTTCTCGGAAGA 910  
 Db 608 CATTTGCCCTTGACCTGAGAACCGAAATGTTACATCCAGGACCAACTTCTCGGAAGA 667  
 QY 911 CGTGTCTATTTTATGTTGACCTCAGTGGCAGCATGAAGAAGCACTCCGCTGACTATCGCGAA 970  
 Db 668 CGTGTCTATTTTATGTTGACCTCAGTGGCAGCATGAAGAAGCACTCCGCTGACTATCGCGAA 727  
 QY 971 GCAAGAGTCTCATTCATTTTGTGATACACTTGGGGATGATGACTTCTTCAACATTAATTC 1030  
 Db 728 GCAAGAGTCTCATTCATTTTGTGATACACTTGGGGATGATGACTTCTTCAACATTAATTC 787  
 QY 1031 TTATTAATGAGAGACTTACATATGTGGAACCTTGCTGAATGAACATTTGGTGAAGCCGA 1090  
 Db 788 TTATTAATGAGAGACTTACATATGTGGAACCTTGCTGAATGAACATTTGGTGAAGCCGA 847  
 QY 1091 CAGGACAAACAAAGAGACACTTCAAGGAGCATCTGAGACAAACTTTTGGCCAAAGGAATTCG 1150  
 Db 848 CAGGACAAACAAAGAGACACTTCAAGGAGCATCTGAGACAAACTTTTGGCCAAAGGAATTCG 907  
 QY 1151 AATGTTGATATAGTCTCTGTAATGAGGCGCTTCAACATTTCTGAGTATTCACACACGCGG 1210  
 Db 908 AATGTTGATATAGTCTCTGTAATGAGGCGCTTCAACATTTCTGAGTATTCACACACGCGG 967  
 QY 1211 ACAAGGAAATATCTGAGTCAGGCGCATCATGCTCATTAATCTGATGGGCGGTGACACCTTA 1270  
 Db 968 ACAAGGAAATATCTGAGTCAGGCGCATCATGCTCATTAATCTGATGGGCGGTGACACCTTA 1027  
 QY 1271 TGTATCAATCTTTGCAAAATACATATTGGCCAGATCGAAGGTTTGCATCAATACCT 1330  
 Db 1028 TGTATCAATCTTTGCAAAATACATATTGGCCAGATCGAAGGTTTGCATCAATACCT 1087  
 QY 1331 CATTTGACGAGAGGCTGCGTTTGCAGACAAATCTAAAGTGGATGGCGTGGCCAAAGAG 1390  
 Db 1088 CATTTGACGAGAGGCTGCGTTTGCAGACAAATCTAAAGTGGATGGCGTGGCCAAAGAG 1147  
 QY 1391 ATTTTATACCCAGATCTCCACCTTTGGCTGATGTGACAGAGAAATGTCAATGAAATACCTTCA 1450  
 Db 1148 ATTTTATACCCAGATCTCCACCTTTGGCTGATGTGACAGAGAAATGTCAATGAAATACCTTCA 1207  
 QY 1451 CGTGTCTACCGGCGCCAAAGTCTATGACACAGAGCATGATGTGCTGACACGACGCTTA 1510  
 Db 1208 CGTGTCTACCGGCGCCAAAGTCTATGACACAGAGCATGATGTGCTGACACGACGCTTA 1267  
 QY 1511 CATTTGACGACACT-----CTGACTGATGATGACAGGCGCGCTGCTGAT 1552  
 Db 1268 CATTTGACGACACTTCTCCTCAGGACAAAGGCTGACTGATGATCAGGCGCGCTGCTGAT 1327  
 QY 1553 GACCACTGTAGCCATGCTCTGTGTTAGTAAGCAGAAAGCAAGACAGATTCGAAGGCAATTC 1612  
 Db 1328 GACCACTGTAGCCATGCTCTGTGTTAGTAAGCAGAAAGCAAGACAGATTCGAAGGCAATTC 1387  
 QY 1613 TCTGGAGAGTGTGGCAGACAGATGTCCCACTGAAGAAGCACTTCTGAAAGCATTCCCAATA 1672  
 Db 1388 TCTGGAGAGTGTGGCAGACAGATGTCCCACTGAAAGCACTTCTGAAAGCATTCCCAATA 1447

QY 1673 CAAAGTTAGGATTCACGGTTATGCTTTGCAATCACAATAATATGRTATATCCGACGCA 1732  
 Db 1448 CAAAGTTAGGATTCACGGTTATGCTTTGCAATCACAATAATATGRTATATCCGACGCA 1507  
 QY 1733 TCCGGAAGTACAGGCTGCTGTACGAAGAAGAAAAAAGCGAAGAAACCTAATATAGTAG 1792  
 Db 1508 TCCGGAAGTACAGGCTGCTGTGTACGAAGAAGAAAAAAGCGAAGAAACCTAATATAGTAG 1567  
 QY 1793 CGTTGACCTCTCTGAGGTGAGTGGGAAGACCGAGATGACGTGTGGAATGCTATGTT 1852  
 Db 1568 CGTTGACCTCTCTGAGGTGAGTGGGAAGACCGAGATGACGTGTGGAATGCTATGTT 1627  
 QY 1853 GAATCGAAGACGGGGAGTTTCCATGAGAGGTGAAGAAGACAGTGGACAAAGGGAAG 1912  
 Db 1628 GAATCGAAGACGGGGAGTTTCCATGAGGTGAAGAAGACAGTGGACAAAGGGTACA 1687  
 QY 1913 GGTAT 1917  
 Db 1688 TTTT 1692

RESULT 14  
 AAS17582  
 ID AAS17582 standard; cDNA; 3445 BP.  
 XX  
 AC AAS17582:  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel secreted protein #11.

KW Secreted protein; cytosolic; immunosuppressive; vulnary; vaccine;  
 KW antiinflammatory; neuroprotective; nephrotoxic; cardiovascular;  
 KW human; cancer; autoimmune disease; wound healing disorder; infection;  
 KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal; ss.

OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..345 /tag= a  
 FT /product= "Human secreted protein"  
 FT

PN WO200179454-A1.  
 PD 25-OCT-2001.

PF 11-APR-2001: 2001WO-US11797.  
 PR 13-APR-2000: 2000US-196603P.  
 PR 24-APR-2000: 2000US-199417P.

PA (SMK ) SMITHKLINE BEECHAM CORP.  
 PA (SMK ) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdoch PR, Ritzvi SK, Smith RF, Xiang Z;  
 DR WPI: 2002-061975/08.  
 DR P-PSDB: AAU09870.

PT New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, cancer

PS Claim 2: page 42-44; 92pp; English.

CC The invention relates to an isolated novel secreted polypeptide (I) and  
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,  
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic  
 CC disorders, inflammatory disorders, infertility, neurological and





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OY 2161 GCAAGAACCTCTGCTCCAGTGTGATAAAGATTGATCCAGAAAGTCCCTTTTGGACGGG 2220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2081 GGAAGAGACCCAGACCTGGAGTGTGACGAGAGCTGTCCGGAGAGTGTGTTTGGACGGG 2140
OY 2221 TGGTGAAGTCCCCCATTTGAAAGCTATTGGACACCTGCGCCCTCAACAATCTGAAATTT 2280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2141 TGGTGAAGTCCCCCATTTGAAAGCTATTGGACACCTGCGCCCTCAACAATCTGAAAGT 2200
OY 2281 CTGACAAAGGCGGTGAGAGTTCTCTCCGACACCTGCGGCGCTCCGCAATCAACC 2340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2201 CTGAAACAGTGTGTGACATGAGCTCTTCTGGACACCTGCGGCTGCTCTGAAAGAGCT 2260
OY 2341 TGTTCGCGGGGCTGACAGCTACCAATAGAGATTCTGAAAGCTGCGCAGCAAGAGA 2400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2261 TGTTCGCGGGGCTGACAGCTACCAATAGAGATTCTGAAAGCTGCGCAGCAAGAGA 2320
OY 2401 ACATTTTAAAGCAGACCATTTTCCCTCTGTGTACCGAAGACCGCTGACGATTCAG 2460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2321 GCGGTTCACCTGGAGCCGCTTCCGCTGTGTACCGCAGGAGCTCAGAGCATCTGCTG 2380
OY 2461 GAGCTTCTCTACTGATCCCATTTAGCACTGAGCAGCTCA-----ATTAAGCAATG 2514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2381 GAGCTTCTCTACTGATCCCATTTAGCACTGAGCAGCTCA-----ATTAAGCAATG 2440
OY 2515 TGGTGAAGCAGATGATCCATCCAGCTCTGATGAAGCAATCTCTGTGGTGAG 2574
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2441 TGGTGAAGCAGATGATCCATCCAGCTCTGATGAAGCAATCTCTGTGGTGAG 2500
OY 2575 CTGTAGGCAATGATCAATCAATTTTCCAAAGAAATCTGTGAGCTGCGCAGCAGAC 2634
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2501 CCGCGGGCTCAAAATGATCAATTTCTCAGCGCAATTTCTCGCGCGCAACCGCGG 2560
OY 2635 AGTGTGCTTCCCTGATGCGCAATGCTCCATCAGCTGTGATGAGACTGTGAATGTT 2694
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2561 AGTGTGCTTCCCTGATGCGCAATGCTCCATCAGCTGTGATGAGACTGTGAATGTT 2620
OY 2695 ACCTCATAGCAATTAATGATTTATTTTGTGTCTGAAGACTACACAGAGTGAAGACT 2754
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2621 TCGTCATCGACAAACAGGGGTTCATTCATTCGAAGAGTCCCGAGACCGGAAGAT 2680
OY 2755 TTTTGGTGAATGAGGAGGAGCTGTGATGAACAATTTGCTAACATGAGCTCTTTAAA 2814
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2681 TTTTGGTGAATGAGGAGGAGCTGTGATGAACAATTTGCTAACATGAGCTCTTTAAA 2740
OY 2815 GAATTAACCTTTATGACTACCAAGCATGTGTAGAGCAACAGGAAGAGGATGAGG 2874
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2741 AGTGTACTATGTATGACTATACAGCCATGTGCAACCCCTGAGTCAACACACAGTGCAG 2800
OY 2875 CCGATGCGCTCTGATCCTTATATGCTTCTCTGCAATGAATGATGATGACAG 2934
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2801 CCGATGCGCTCTGATCCTTATATGCTTCTCTGCAATGAATGATGATGACAG 2860
OY 2935 AACTGTCTTGTCCGAGGGAATTTAACTCTGCAAGTGTGTGCACTCCGATATGACAG 2994
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2861 AACTGTCTTGTCCGAGGGAATTTAACTCTGCAAGTGTGTGCACTCCGATATGACAG 2920
OY 2995 CTAAAGCCCAAGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3051
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2921 AGGCCCAAGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2980
OY 3052 TGGTCTGTGAGGAGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2981 TGGTCTGTGAGGAGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3040
OY 3112 ACTCTTTTGTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3171
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3041 AGGATTTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3100
OY 3172 GCGTGCCTGTG---TGAATCTGTGCGCCCATCAACATGAGCAGCAATGAATCAGATATA 3228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3101 CCTTCTGAGAGATGGGCTCCGCTCTGAGATATTGACCTTAACAGAGTGGCTTCTGACATA 3160

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OY 3229 ATGATCCCTTAAGTGTGAACGCTTAAAGGCCAGAGATCAGAGAGGCCAGATCTT 3288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3161 ATGCTCTGTCAATATGTACCGGATGCGCTCCCAAGAGCTCCGCCGACCAATCTCT 3220
OY 3289 GTCATGCTTCAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3221 GCCAGGCTTTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3280
OY 3349 CCCAGAGAGTCTCTCTCTGCTCCCTCTG 3377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3281 CCTGCGCGCCCTCTACTCTCTGCTGTG 3309

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RESULT 15
AAA09254
ID AAA09254 standard; cDNA; 5073 BP.
XX
XX AAA09254;
AC
XX
XX 10-AUG-2000 (first entry)
DT
XX
DE Human alpha-2-delta-D gene.
XX
XX alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytosolic;
KW anticonvulsant; antimigraine; antiparkinsonian; antidepressant; ss.
XX
XX Homo sapiens.
OS
PH
FH Key Location/Qualifiers
FT CDS 3..3365
FT /*tag= a
XX
XX MO200020450-A2.
XX
XX 13-APR-2000.
PD
XX
XX 07-OCT-1999; 99WO-US23519.
PF
XX
XX 07-OCT-1998; 98US-010322.
PR 30-OCT-1998; 98US-010673.
PR 29-DEC-1998; 98US-0114088.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
PI John MA, Moldover B, Offord JD;
XX
XX WPI: 2000-303744/26.
XX
XX P-PSDB: AAY92321.
XX
XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
XX proteins, useful in the treatment of epilepsy, migraine, chronic pain,
XX anxiety, multiple sclerosis or cancer
XX
XX Claim 1: Page 64-66; 88pp; English.
XX
XX The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
XX The gene has been mapped to chromosome 12p13.1. This gene and the related
XX alpha-2-delta-C and -B genes are useful for protecting mammalian cells
XX from abnormal calcium flux by introducing expression vectors containing
XX the respective gene into mammalian cells. The antisense genes are also
XX useful for treating or preventing epilepsy. The alpha-delta-2-A protein
XX is a high-affinity binding target of the anti-convulsant drug gabapentin.
XX Therefore, alpha-delta-2 proteins may also be targeted to treat
XX seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
XX pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
XX multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
XX addiction syndromes, mood, depression or cancer.
XX
XX Sequence 5073 BP; 1280 A; 1390 C; 1347 G; 1056 T; 0 other:
SQ

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Query Match 33.6%; Score 1268.2; DB 21; Length 5073;
Best Local Similarity 63.6%; Pred. No. 1.5e-277;
Matches 2015; Conservative 0; Mismatches 1113; Indels 39; Gaps 4;

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QY	250	AGATTCACCGCTCTCCGTGTGAAGCTCTGGGCTCGGGCTTTTGTGGGGAGATTAATAATCCA	309
Db	163	AGATTCCTCTGGAAACAGTGAAGCTATGGGCTGACACCTTGGGGGGGACCTGTATATACA	2222
QY	310	TTTGCTCTAAGTACTCCGTTTCCAGCTTCTGCAAAAGAAATACAAAGAATATGAGAAG	369
Db	223	CTGTGACCAAAATCTACAGGCTCTCTCTTCTGTGCAGAAAGAAATACAAAGATGTGGATGCCA	282
QY	370	ACGTTGCCATTAAGAAATATGATGGCCCTCCAACTGGTAAAGAACTGGCAAGAACACTGG	429
Db	283	GTCTGAAGTTCAGAGAGCTGGATGGCTTTGAGCTGTGGTAGAAATTTCTCAGAGACATGG	342
QY	430	AAGAGATGTTTTCACAAGAAGTCTGAGGCCCTGAGGCGCTGTGTGGAGCTTCAGAAATAG	489
Db	343	AGAACTAGCTGGGAGGAAAGTCCAGGGCGGTCCAGAAATCTGTGTGAAGCTTCCGAGAGG	402
QY	490	CACACCTTAACATCAATTTGATGACAGCTTACAGTATGAATTAATCTCAATGCTGTGTGA	549
Db	403	CCGACCTGAACCAACAAATTCATGAAATCCCTGTGTTCGACTATTACAACTCGCTCTGTA	462
QY	550	TAAATGAAAGGACCAAGAACGGGAATTTTTTGGAGCTGGGAAAGAAATTTATCTTAACC	609
Db	463	TCAAGGAGAGGAGACAGAAAGGCAACTTCGTGGAGCTGGGCGCCGCAATTCCTCTGGAGT	522
QY	610	CAAATGACCATTATTAATTTGGCTGTGAACATCACTTAAGTAGAGCTCCAAATACCA	669
Db	523	CCAAATGTCACCTTGAGCAACCTGGCGGTGAACACCTCCATTCAGAGGTCTACCTGCCA	582
QY	670	CGAATATGTACCAAGAACCCCTGCATTTGTCAATGGGGTTTATGGTCTGAATCTCTAA	729
Db	583	CCAAAGGTGTACAAACAAACCCCAATATTTAAATGAGTCTCAATGTCTGAAGCTCTTG	642
QY	730	ACAAGTTTTTGTGATATCTTACCGTAGACCCATCTCATATGGCAATCTACTTTGGAA	789
Db	643	ATGCTGTCTTGTGGAGAACTTCCAGAGAGACCCCAACGTTTGACCTGGCAATATTTGGCA	702
QY	790	GTGCAAGGGCTTTTTTAAAGCAGTATCCGGGATTTAAATGGGAACCAAGATGAGATGGAG	849
Db	703	GTGCAACTGTGATTTCTTGAGATCTATCCAGGATTAATAATGGACACCTGATGAGAAATGGAG	762
QY	850	TCATTGGCTTGGACTGCAAGAACCGAAATGTGTATCCAGGACGACACTTCCGAAAG	909
Db	763	TCATTACTTTGACTGGCGAAACCGCGGTGTATCAATCAAGCTGTACTTCCCAAG	822
QY	910	ACGTGCTATTTTGTGTGAGCTGCTGCTGGAGCAAGAAAGACCTCCGTCATCTATGCGCA	969
Db	823	ACATATGTATTTTGTGTGAGCTGCTGCTGGAGCAAGAAAGGCTGAGCAATCTATTTGCCA	882
QY	970	AGCAAAAGCTCTCATCTATTTTGGATACATTTGGGATGATGATCACTTCAACATTAATG	1022
Db	883	AGCAACACCATCAACCATCTTGGACACCTTGGGGGAGAAATGACTTGTGTAATATCANTAG	942
QY	1030	CTTATATGAGAGCTTCACTATGTGGAACTTGTGCTGAATGGAACTTTGTGCAAGCG	1088
Db	943	CGTCAATATGACTACGTCAATTAATCATGAGCGCTTTTAAAGGATCCATGTGCAAGCGG	1002
QY	1090	ACAGAGAACCAAAAGACCACTTCAAGGAGAGATGTGGACAACTTTTCCGTAAGGAATTG	1144
Db	1003	ACCGAGACAATCGAGACATTTTAACTGTGTGGAGAGATTTGAATGGTCTAAAGGTGTGG	1067
QY	1150	GAATGTTGATATAGCTCTGAATGAGGCGCTTCAACTCTGATGTGTTTCAACCAACAGG	1209
Db	1063	GGGTCTGTGACCAAGCCCTGAGGAAGCCCTTCCAGATCTGAAAGCAGTTTCAAGAGGCCA	1122
QY	1210	GACACGAAATATCTGCAATGTCAGGCCATCACTGCTCAATCACTAGATGGGGCTGTGACACT	1265
Db	1123	AGCAAGAGAAAGCTCTGCAACCAAGGCATCATGCTCATCGACACGGCGCTGTGGAGACT	1188
QY	1270	ATGATTAACAATCTTTGCAAAATTAATTTGGCGAGATGGAAGGTTGGCATTTTCACATACC	1329
Db	1183	ACGAGCCGGGTGTTGAGAACTATTAATCTGGCGAGACGTGAATGTCCGAGTTTCTACCTTACC	1242

[illegible]

Db 2323 GCGTGTTCACCCCTGGACCGCTTCCCGCTGTGTACCCGCGCCTCAGACATCTCTGCTG 2382  
 QY 2461 GGAGCTTGTCTACTGATCCCATTCAGACACTGACAGTCA-----ATAAAGCAATG 2514  
 Db 2383 GCACCTTGTCTTCAACCTCCGCTGGGCAAGACACAGAAAGTGGGGTGAAACCATGG 2442  
 QY 2515 TGGTGACAGCAAGTACATCCAGCTCCTGTGATGAACGGAATCTCTGTGTGGCAG 2574  
 Db 2443 TGGTGACGGCAAGCAGACACTGTGGGGTGACCTGGACAAAGAGCAGACCATTTGCTGCAG 2502  
 QY 2575 CTGTAGGCAATTCAGATGAATTTTTCAAAGGAAGTTCTGACTCCAGCAGAC 2634  
 Db 2503 CCGCGGGGCTCCAATATGAAGTGAATTCCTCAGCGCAATTCGGGGGCGCAACGCGGC 2562  
 QY 2635 AGTGTGCTTCCCTGGATGGCAAAATGCTTCATCAGCTGTGATGATGAGACTGTGAATGTT 2694  
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 QY 2695 ACCTCATAGACAAATATGATTTTATTTTGTGTGAAGACTACACACAGACTGGAGACT 2754  
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 QY 2755 TTTTGTGAGATCGAGGAGGAGCTGTGATGAACAATTTGCTAACATGGGCTCTTTAAA 2814  
 Db 2683 TTTCTGGGGAGGTGATGTGTCTCTGACCCAGCTGCTCAGCATGGGGGTGTTCAACC 2742  
 QY 2815 GAATTACCTTTTATGATACCAAGCCATGTGTAGAGCCAAAGAAAGAGAGCGATGGCG 2874  
 Db 2743 AAGTACTATATGATATGACCCATGACCAATGCAAAACCTCGAGTCAACACAGTGCAG 2802  
 QY 2875 CCCATGGCTCTCTGATCTTATATGCTTCTCTGAGTAATAATGATCATGACAG 2934  
 Db 2803 CCCAGCCCCGTGTGACGCCCAATTTCTCTTGTGACGGGACAGGTGGCTGCTGCAGG 2862  
 QY 2935 AACTTGTCTTGTCTGTGTGAAATTAACCTGTGAGTTGTGCACTCCGATATGACAG 2994  
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 Db 2923 AGCCCAAAAGTGTCTTCCATCACTCCCAACAAAGAGAGAGACCCGCTCAGCCCT 2982  
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 QY 3151 TCATGGTGTGGGACAGCAGCTGCTGTGTGATCTGTGGCCCCCATCACCATGCGAC 3210  
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 QY 3211 CCATTGAATCAGGTATATGATCCCTTAAGTGAAGCTTAAGGCGCAGAAAGATCA 3270  
 Db 3163 CGACAGAGTCAAAATATATATGCTGTGTCAATGTGACCGGATGCGCTCCGAAAGCTCC 3222  
 QY 3271 GAAGGCGCCCAAGATCTGTGTGATGCTGTGATGATGAGAGAAATGCAAGGAGTGGGG 3330  
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 QY 3331 GTGCGCGAGTCTCCAGGCCCAAGAGTCCCTTCTGCTCTG 3377  
 Db 3283 GCGCTCGACACCTCAGGCTGCGCGCCCTTACTCTGTCTGTG 3329

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2003, 23:59:56 ; Search time 403 seconds

(without alignments)  
10179.269 Million cell updates/sec

Title: US-09-787-657-3

Perfect score: 3770

Sequence: 1 tactataggcgccgcgaa.....aaaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 segs, 544064369 residues 1419640

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 12: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3604.8	95.6	3690	US-10-162-012-14	Sequence 14, Appl
2	3604.8	95.6	3690	US-09-875-423-1	Sequence 1, Appl
3	3378.2	89.6	3528	US-09-728-628-12	Sequence 12, Appl
4	3229.6	85.7	3276	US-10-162-012-16	Sequence 16, Appl
5	3229.6	85.7	3276	US-09-875-423-3	Sequence 3, Appl
6	419	11.1	519	US-09-563-817-794	Sequence 794, App
7	387.2	10.3	667	US-09-924-340-99	Sequence 99, Appl
8	387.2	10.3	667	US-09-992-600A-99	Sequence 99, Appl
9	214	5.7	5463	US-10-116-949-1	Sequence 1, Appl
10	214	5.7	5463	US-10-116-949-3	Sequence 1, Appl
11	206.4	5.5	5279	US-10-116-949-5	Sequence 5, Appl
12	135.4	3.6	1217	US-10-050-786-4	Sequence 4, Appl
13	130.6	3.5	3055	US-10-090-827-11	Sequence 10, Appl
14	130.6	3.5	3109	US-10-090-827-11	Sequence 11, Appl
15	130.6	3.5	3190	US-10-090-827-12	Sequence 12, Appl
16	130.6	3.5	3600	US-10-090-827-17	Sequence 17, Appl
17	113	3.0	3057	US-10-090-827-2	Sequence 2, Appl
18	113	3.0	3111	US-10-090-827-3	Sequence 3, Appl
19	113	3.0	3192	US-10-090-827-4	Sequence 4, Appl

## ALIGNMENTS

20	113	3.0	3842	US-10-090-827-1	Sequence 1, Appl
21	107.6	2.9	503	US-10-050-786-5	Sequence 5, Appl
C 22	61.8	1.6	456	US-09-864-761-11292	Sequence 11292, A
C 23	59.2	1.6	168	US-09-864-761-27992	Sequence 27992, A
24	53.4	1.4	1614	US-09-976-740-45	Sequence 45, Appl
25	53.4	1.4	1614	US-10-023-529-45	Sequence 45, Appl
26	53.4	1.4	1614	US-10-023-529-45	Sequence 45, Appl
27	53.4	1.4	12425	US-09-976-740-50	Sequence 50, Appl
28	53.4	1.4	12425	US-10-023-529-50	Sequence 50, Appl
29	53.4	1.4	12425	US-10-023-529-50	Sequence 50, Appl
30	52.6	1.4	1500	US-09-917-800A-1333	Sequence 1333, Ap
31	51.2	1.4	2561	US-09-976-740-48	Sequence 48, Appl
32	51.2	1.4	2561	US-10-023-529-48	Sequence 48, Appl
C 33	51.2	1.4	2561	US-10-023-529-48	Sequence 48, Appl
C 34	51	1.4	1662	US-09-922-862-1	Sequence 1, Appl
C 35	50.2	1.3	43058	US-09-954-456-292	Sequence 292, App
C 36	50.2	1.3	43058	US-09-954-456-529	Sequence 529, App
C 37	50.2	1.3	43058	US-09-954-456-529	Sequence 3950, Ap
C 38	50	1.3	8147	US-10-109-886-9	Sequence 9, Appl
C 39	49.8	1.3	3116	US-09-855-754-3	Sequence 3, Appl
40	48.2	1.3	2307	US-09-893-519A-87	Sequence 87, Appl
C 41	47.8	1.3	419	US-09-960-352-11234	Sequence 11234, A
C 42	47.6	1.3	10464	US-09-957-974-1	Sequence 1, Appl
C 43	47.6	1.3	53522	US-09-904-968A-1	Sequence 45, Appl
C 44	47.2	1.3	1614	US-09-976-740-45	Sequence 45, Appl
C 45	47.2	1.3	1614	US-10-023-529-45	Sequence 45, Appl

RESULT 1  
US-10-162-012-14  
Sequence 14, Application US/10162012  
Publication No. US20030051660A1  
GENERAL INFORMATION:  
APPLICANT: Curtis, Roy A.J.  
APPLICANT: Sltos-Santlago, Inmaculada  
APPLICANT: Gu, Wei  
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS  
FILE REFERENCE: 10448-190001  
CURRENT APPLICATION NUMBER: US/10/162,012  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 60/209,845  
PRIOR FILING DATE: 2000-06-06  
PRIOR APPLICATION NUMBER: US 09/875,321  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: PCT/US01/18340  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: US 60/209,257  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: US 09/875,423  
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PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/209,238  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: US 09/875,363  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: PCT/US01/18247  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/227,068  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: US 09/928,530  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: PCT/US01/25475  
PRIOR FILING DATE: 2001-08-15  
PRIOR APPLICATION NUMBER: US 60/226,770  
PRIOR FILING DATE: 2000-08-21  
PRIOR APPLICATION NUMBER: US 09/934,421  
PRIOR FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: PCT/US01/26096  
PRIOR FILING DATE: 2001-08-21

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: PRIOR APPLICATION NUMBER: US 60/279,281
: PRIOR FILING DATE: 2001-03-28
: PRIOR APPLICATION NUMBER: US 10/109,029
: PRIOR FILING DATE: 2002-03-28
: PRIOR APPLICATION NUMBER: PCT/US02/09728
: PRIOR FILING DATE: 2002-03-28
: PRIOR APPLICATION NUMBER: US 60/290,288
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: US (not assigned)
: PRIOR FILING DATE: 2002-05-13
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 3690
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (29)...(3301)
: US-10-162-012-14
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Best Local Similarity 99.4%  Pred. No. 0;
Matches 3631;  Conservative 3;  Mismatches 0;  Indels 18;  Gaps 1;
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Db 22 GCCCAGCAGTGGCCGGCCGCTCCGCCGCCGCTCCCGGGGGGCTCGGCGCTTCT 81
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RESULT 2
US-09-875-423-1
: Sequence 1, Application US/09875423
: Patient No. US2002081657A1
: GENERAL INFORMATION:
: APPLICANT: Curfiss, RORY A.J.
: TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
: FILE REFERENCE: 10448-059001
: CURRENT APPLICATION NUMBER: US/09/875,423
: PRIOR APPLICATION NUMBER: 2001-06-05
: PRIOR FILING DATE: 2000-06-05
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3690
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (29)...(3301)
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Db	2182	TTTCGACAAAGGCGCGTGAAGGTTCGCTTCCTGGCACTCGACGGGCTCTCCAGAAATCAA	2241
QY	2339	CCTGTTTGTGGGGGCTGAGCACTCACCAAATCAGAGACTCCTGAAAGTGGCGCAAGGA	2398
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QY	2399	GAACATTTTAAAGCAGACCAATTTCCCTCTCTGTAGCGAAGAGCCGCTGAGCAGATTC	2458
Db	2302	GAACATTTTAAAGCAGACCAATTTCCCTCTCTGTAGCGAAGAGCCGCTGAGCAGATTC	2351
QY	2459	AGGAGCTGTGTCTACTGCTGATCCCATTCAGACACTGACACGTCAATTAAGCAATGTGT	2518
Db	2362	AGGAGCTGTGTCTACTGCTGATCCCATTCAGACACTGACACGTCAATTAAGCAATGTGT	2421
QY	2519	GACAGCAAGTACATCCATCCAGCTCCGAGTGAAGAGAAATTCCTGTGGTGGAGCTGT	2578
Db	2422	GACAGCAAGTACATCCATCCAGCTCCGAGTGAAGAGAAATTCCTGTGTGGAGCTGT	2481
QY	2579	AGGCATTCAGATGAATCTGAATTTTCCAAAGGAATTCGTGCACTGCCAGCAGACAGT	2638
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	Db	3202	CCATCTGTGAGGAATGCAGGGAATGTGGGGTGGCGCATCTCCCAAGGCCACAGCAGT	3261
OY	3359	CCCTCTTGTCGCCCTCTGCTTTTATGCTCTCTTCAAGAGTGACACTAGATGATTTC		3418
Db	3262	CCTCCTTGTCGCCCTCTGCTTTTATGCTCTCTTCAAGAGTGACACTAGATGATTTC		3321
OY	3419	TCTTACTAGTAGATGATTGTTCTCTTGGCATGCTAAATCATGATAAAGTGTACCANAAT		3478
Db	3322	TCTTACTAGTAGATGATTGTTCTCTTGGCATGCTAAATCATGATAAAGTGTACCANAAT		3381
OY	3479	ATGTGTCAACATACGACACATGATATATGTCCAACATCACATCTCATCTGATTTTTAA		3538
Db	3382	ATGTGTCAACATACGACACATGATATATGTCCAACATCACATCTCATCTGATTTTTAA		3441
OY	3539	ACTGTGCTGATATTAACCTCTTAAAGATATGTACAANAAGTATATCATCTTTTAA		3598
Db	3442	ACTGTGCTGATATTAACCTCTTAAAGATATGTACAANAAGTATATCATCTTTTAA		3501
OY	3599	CTTGGCAGTCATGCATATGTAGTGTGGCCATGATATACCCCTTCATCAGAAATGGG		3658
Db	3502	CTTGGCAGTCATGCATATGTAGTGTGGCCATGATATACCCCTTCATCAGAAATGGG		3561
OY	3659	ACCCCAAGTGTAGGCAAGTGTCCCTTCTGCTTGAACCTATTTGAACCAATTTAAAAGT		3718
Db	3562	ACCCCAAGTGTAGGCAAGTGTCCCTTCTGCTTGAACCTATTTGAACCAATTTAAAAGT		3621
OY	3719	TGTACTTTTAAATTAAGTATATTTAAATATCTTAAAAAAGTATTTAAAAA		3770
Db	3622	TGTACTTTTAAATTAAGTATATTTAAATATCTTAAAAAAGTATTTAAAAA		3673
 RESULT 3 US-09-728-628-12				
	/ Sequence 12, Application US/09728628			
	/ Patent No. US2002009786A1			
	GENERAL INFORMATION:			
	APPLICANT: Tang, Y. Tom			
	APPLICANT: Zhou, Ping			
	APPLICANT: Goodrich, Ryle			
	APPLICANT: Liu, Chenghua			
	APPLICANT: Asundi, Vinod			
	APPLICANT: Xue, Aidong J.			
	APPLICANT: Zhang, Jie			
	APPLICANT: Zhao, Qing A.			
	APPLICANT: Ren, Feiyang			
	APPLICANT: Drmanac, Radoje T.			
	TITLE OF INVENTION: No. US2002009786A1el Nucleic Acids and			
	FILE REFERENCE: 79JCIP2C			
	CURRENT APPLICATION NUMBER: US/09/778, 628			
	CURRENT FILING DATE: 2000-12-01			
	PRIOR APPLICATION NUMBER: 09/552, 929			
	PRIOR FILING DATE: 2000-04-18			
	NUMBER OF SEQ ID NOS: 14			
	SOFTWARE: pt_FL-genes Version 2.0			
	SEQ ID NO 12			
	LENGTH: 3528			
	TYPE: DNA			
	ORGANISM: Homo sapiens			
	FEATURE:			
	NAME/KEY: CDS			
	LOCATION: (213) . (3206)			
	US-09-728-628-12			
 Query Match            89.6%; Score 3378.2; DB 10; Length 3528; Best Local Similarity   98.4%; Pred. No. 0; Matches 3458; Conservative   1; Mismatches     9; Indels     45; Gaps       3;				
OY	256	CGCTCTCCGTGCTGAAGCTCTGGAGCTCGGCTTTGTGGGAGAGATTAATCCATTGGCG		315
Db	43	CTCCCTGTAGAGTGAAGCTCTGGAGCTCGGCTTTGTGGGAGAGATTAATCCATTGGCTG		102

QY	316	CTAAGTACTCGGGTTCCTCCAGCTTCTCGCAAAAGAAATCTCAAAGATATGAGAAAGACGTTG	375
Db	103	CTTAAGTACTCCGGTTCCTCCAGCTTCTCGCAAAAGAAATCTCAAAGATATGAGAAAGACGTTG	162
QY	376	CCATAGAAAGAAATTTATGATGGCTCCCAACTGATGAAGAAGCTGGCAAAACATGATGAAGAGA	435
Db	163	CCATGTAAGAAATTTATGATGGCTCCCAACTGATGAAGAAGCTGGCAAAACATGATGAAGAGA	222
QY	436	TGTTTTACAGAAGATCTGAGGCCCTCAGCCCTCTGTGGAGGGCTGCAAGAAAGACACCC	495
Db	223	TGTTTTACAGAAGATCTGAGGCCCTCAGCCCTCTGTGGAGGGCTGCAAGAAAGACACCC	282
QY	496	TGAAACATGAATTTATGATGCAGACTTACAGATATGAATACTTCAATGCTGTGCTATTAATG	555
Db	283	TGAAACATGAATTTATGATGCAGACTTACAGATATGAATACTTCAATGCTGTGCTATTAATG	342
QY	556	AAAGGACAAAGACCGGAATTTTTTGGAGCTGGGAAGAAGAAATTCATCTTAGCCCCAATG	615
Db	343	AAAGGACAAAGACCGGAATTTTTTGGAGCTGGGAAGAAGAAATTCATCTTAGCCCCAATG	402
QY	616	ACCATTTTAAATTAATTTGCCCTGTGAACATCACTAAGTGAAGTCCAAAGTACCAACAGACA	675
Db	403	ACCATTTTAAATTAATTTGCCCTGTGAACATCACTAAGTGAAGTCCAAAGTACCAACAGACA	462
QY	676	TGTACAAACAAAGACCCCTGCATTTGTCAATGTGGGCTTATTTGGTGTGAATCTCTTAACAAAG	735
Db	463	TGTACAAACAAAGACCCCTGCATTTGTCAATGTGGGCTTATTTGGTGTGAATCTCTTAACAAAG	522
QY	736	TTTTTTGTAGATTAACCTTTGACCGGTGACCCATCTCTCATATGGCAGTACTTTTGGAAATGCAA	795
Db	523	TTTTTTGTAGATTAACCTTTGACCGGTGACCCATCTCTCATATGGCAGTACTTTTGGAAATGCAA	582
QY	796	AGGGCTTTTTTAAAGCAGTATCCGGGGATTAAATGGAACACAGATGAGAAATGGAATCATTG	855
Db	583	AGGGCTTTTTTAAAGCAGTATCCGGGGATTAAATGGAACACAGATGAGAAATGGAATCATTG	642
QY	856	CCTTGAGCTGCAAGAACCGAAATATGATATCCAGAGCAACTTCTCCGAAAGACGTGG	915
Db	643	CCTTGAGCTGCAAGAACCGAAATATGATATCCAGAGCAACTTCTCCGAAAGACGTGG	702
QY	916	TCATTTTATGTTGAGCTGAGTGGCAGCATGAAAGAGACTCCGTCTGACTATTCGGGAAGCAAA	975
Db	703	TCATTTTATGTTGAGCTGAGTGGCAGCATGAAAGAGACTCCGTCTGACTATTCGGGAAGCAAA	762
QY	976	CAGTCTCATTCATTTTGGATATACACTTGGGAGTATGACTTCTTCAACATTAATTTGCTTATA	1035
Db	763	CAGTCTCATTCATTTTGGATATACACTTGGGAGTATGACTTCTTCAACATTAATTTGCTTATA	822
QY	1036	ATGAGGACCTTCACTATGTGGAACCTTGGCTGAAATGGAACCTTGGTGGCAAGCCGACAGGA	1095
Db	823	ATGAGGACCTTCACTATGTGGAACCTTGGCTGAAATGGAACCTTGGTGGCAAGCCGACAGGA	882
QY	1096	CAAAACAAAGACACTTTCAGGAGACATCTGACAAACTTTTTCGCAAAAGAAATTTGGAATGT	1155
Db	883	CAAAACAAAGACACTTTCAGGAGAGATCTGACAAACTTTTTCGCAAAAGAAATTTGGAATGT	942
QY	1156	TGATATATAGCTCTGAATGAGGCCCTTCAACTTCTGAGTATTTCAACACACAGGGAGCAAG	1215
Db	943	TGATATATAGCTCTGAATGAGGCCCTTCAACTTCTGAGTATTTCAACACACAGGGAGCAAG	1002
QY	1216	GAAATATCTGCAAGTCAAGGCCATCATGCTCTAATCTATGGGGCGTGGAGCACTATGTATA	1275
Db	1003	GAAATATCTGCAAGTCAAGGCCATCATGCTCTAATCTATGGGGCGTGGAGCACTATGTATA	1062
QY	1276	CAATCTTTGGCAAAATTAACAATTTGGCCAGATGGAAGGTTGGCAATCTTCAATACCTCATTG	1335
Db	1063	CAATCTTTGGCAAAATTAACAATTTGGCCAGATGGAAGGTTGGCAATCTTCAATACCTCATTG	1122
QY	1336	GAGCAGAGGCTGCGTTTGGCAGACAAATCTAAAGTGAATGGCTGTGCCCAAAACAAAGATTTT	1395
Db	1123	GAGCAGAGGCTGCGTTTGGCAGACAAATCTAAAGTGAATGGCTGTGCCCAAAACAAAGATTTT	1182
QY	1396	TTACCCAGATCTCCACTTTGGCTGATGTGCAAGAGAAATGTCAATTAACCTTCACTGTC	1455

[illegible]

Db	2263	CAGGAGCTTGTCTACTCCGATCCCATTCACGACTGGACCGTCAATTAATAAGCAATGTGG	2322
Qy	2518	TGACAGCAAGTACATCCATCCAGCTCTCTGATGAACGGAAATCTCTGTGGTGGCAGCTG	2577
Db	2323	TGACAGCAAGTACATCCATCCAGCTCTCTGATGAACGGAAATCTCTGTGGTGGCAGCTG	2382
Qy	2578	TAGCATTCAGATGAACCTGGAATTTTTCCAAAGGAAGTTCTGGACTG(C)CAGCAGAGT	2637
Db	2383	TAGCATTCAGATGAACCTGGAATTTTTCCAAAGGAAGTTCTGGACTG(C)CAGCAGAGT	2442
Qy	2638	GTCCTTCCTCGATGGCCAAATGCTCCATCTAGCTGTGATGATGAGACGTAAGTGTATACC	2697
Db	2443	GTCCTTCCTCGATGGCCAAATGCTCCATCTAGCTGTGATGATGAGACGTAAGTGTATACC	2502
Qy	2698	TCATAGCAATPATGATATTTATTTTGGTGTCTGAAGACTACACACATCGAGACTTTT	2757
Db	2503	TCATAGCAATPATGATATTTATTTTGGTGTCTGAAGACTACACACATCGAGACTTTT	2562
Qy	2758	TTGSGTGATCGAGGGAGCGTGATGAACAAATTTGCTAACAAATGGCTCCTTTAAAGAA	2817
Db	2563	TTGSGTGATCGAGGGAGCGTGATGAACAAATTTGCTAACAAATGGCTCCTTTAAAGAA	2622
Qy	2818	TTACCTTTATGACTACCAAGCCATGTGTAGACCAACAAGAGAAGAGATGGGGCC	2877
Db	2623	TTACCTTTATGACTACCAAGCCATGTGTAGACCAACAAGAGAAGAGATGGGGCC	2682
Qy	2878	ATGGCTCTCTGGATTCCTTATATGCTTCTCTCTGACGTAATAATGGATCATGACAGAAC	2937
Db	2683	ATGGCTCTCTGGATTCCTTATATGCTTCTCTCTGACGTAATAATGGATCATGACAGAAC	2742
Qy	2938	TTGTCTGTTTCCGSGGGAATTTAACTCTGCGAGTTGTGTGGCACTCCGATATGACAGTA	2997
Db	2743	TTGTCTGTTTCCGSGGGAATTTAACTCTGCGAGTTGTGTGGCACTCCGATATGACAGTA	2802
Qy	2998	AAGCCAGAAATTTGAACAGACCCTGGAGCCTGTGATACTGTAAATTCAGATTTGCTCT	3057
Db	2803	AAGCCAGAAATTTGAACAGACCCTGGAGCCTGTGATACTGTAAATTCAGATTTGCTCT	2862
Qy	3058	CTGAGCGCACCATCAAGAGACTACAGGAATAATTCCTTGTGAAGCTCTCCAACTGCT	3117
Db	2863	CTGAGCGCACCATCAAGAGACTACAGGAATAATTCCTTGTGAAGCTCTCCAACTGCT	2922
Qy	3118	TTGTGATCCAGAAATCCCAACAGCAACCTGTTCATGTGTGTGTGGACACAGCAGTGC	3177
Db	2923	TTGTGATCCAGAAATCCCAACAGCAACCTGTTCATGTGTGTGTGGACACAGCAGTGC	2982
Qy	3178	TCGTGAATCTGTGGCCCCATCACCATGGACCCCATTAATAATCAAGGTATATGAATCCC	3237
Db	2983	TCGTGAATCTGTGGCCCCATCACCATGGACCCCATTAATAATCAAGGTATATGAATCCC	3042
Qy	3238	TTTAAGTGTGAACGTCTTAAAGGCCAGAAAGATCAGAAGGGGCCAGATCTTCATGTGCT	3297
Db	3043	TTTAAGTGTGAACGTCTTAAAGGCCAGAAAGATCAGAAGGGGCCAGATCTTCATGTGCT	3102
Qy	3298	TCATATCGAGAGAGATGCAAGGGAGTGTGGGGGTGGCCGAGTCTCCAAAGCCAGACAG	3357
Db	3103	TCATATCGAGAGAGATGCAAGGGAGTGTGGGGGTGGCCGAGTCTCCAAAGCCAGACAG	3162
Qy	3358	TCCTTCCTTCTGCTCCCTCTGCTTTTGTATGTCTTCTCAAGGGTGAACAGTACGTGATGTT	3417
Db	3163	TCCTTCCTTCTGCTCCCTCTGCTTTTGTATGTCTTCTCAAGGGTGAACAGTACGTGATGTT	3207
Qy	3418	CTCTTACAGTGAAGATTTCTCTTGGCATCGTAAATCATGGATTAACATGTGAACCAAA	3477
Db	3208	-----ACTGACTGAGATGTTCTCTTGGCATCGTAAATCATGGATTAACATGTGAACCAAA	3262
Qy	3478	TATGATGCAACATAGCAACATGGAATATAGTCCAAACCATCAGCATCTCATGATTTTA	3537
Db	3263	TATGATGCAACATAGCAACATGGAATATAGTCCAAACCATCAGCATCTCATGATTTTA	3322
Qy	3538	AACGTGTGATATTAACCTCTTAAAGATATGTGGACAAAAGTTATCTTCATCTTTT	3597
Db	3323	AACGTGTGATATTAACCTCTTAAAGATATGTGGACAAAAGTTATCTTCATCTTTT	3375

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Oy  3598  ACCTTGCCACTCATGCAAAATGAGATTTGCCATGATAAATCACCCTTCACCAAAATGG  3657
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Db  3376  ACTTTGCCACTCATGCAAAATGAGATTTGCCACATGATAAATCACCCTTCACCAAAATGG  3435
      |||||||
Oy  3558  GACCGCAAGTGTAGGCACTGTCCCTTCGTGTAACCTATTGAACCAATTTAAACT  3717
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Db  3436  GACCGCAAGTGTAGGCACTGTCCCTTCGTGTAACCTATTGAACCAATTTAAACT  3495
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Oy  3718  GTGTACTTTTAAATTAAGTATATTAAATCAT  3750
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Db  3496  GTGTACTTTTAAATTAAGTATATTAAATCAT  3528

RESULT 4
US-10-162-012-16
; Sequence 16, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-162-012-16

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Db	2101	AGTCCCCCATTTGAAGGATTTGGACCAAGCTGGCCCTCAACAAATCTGAAAATTTCTGCAC	2160
QY	2286	AAGGCGTGGAGCTTGCCCTTCTCGGACATTCGACGGGCGCTTCAGAAATCAACCTGTTT	2345
Db	2161	AAGGGGCTGGAGGTTGCCTTCTCTCGGACATTCGACGGGCGCTTCAGAAATCAACCTGTTT	2220
QY	2346	GTGCGGGCTGAGAGCTGCACCAATCAGAGACTTCTCTGAAGCTGGCGACAGAGACAATT	2405
Db	2221	GTGCGGGCTGAGAGCTGCACCAATCAGAGACTTCTCTGAAGCTGGCGACAGAGACAATT	2280
QY	2406	TTTAAAGCAGACCAATTCCCTCTCTGGTACGGAAGACCGCTGAGCAATTCAGGGAGCG	2465
Db	2281	TTTAAAGCAGACCAATTCCCTCTCTGGTACGGAAGACCGCTGAGCAATTCAGGGAGCG	2340
QY	2466	TTTCGTACTCGATCCCATTCAGACACTGACACAGTCAATTAAGCAATCTGTGTACAGCA	2525
Db	2341	TTTCGTACTCGATCCCATTCAGACACTGACACAGTCAATTAAGCAATCTGTGTACAGCA	2400
QY	2526	AGTACATTCATCCAGCTCCTGGATGAACGGAAATCTCTGTGGTGGCAGCTGTAGCAATT	2585
Db	2401	AGTACATTCATCCAGCTCCTGGATGAACGGAAATCTCTGTGGTGGCAGCTGTAGCAATT	2460
QY	2586	CAGATGAACCTGAATTTTCCAAAGGAATTCCTGCACTGCCAGCAGACAGTGTGCTTCC	2645
Db	2461	CAGATGAACCTGAATTTTCCAAAGGAATTCCTGCACTGCCAGCAGACAGTGTGCTTCC	2520
QY	2646	CTGGATGGCAAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTTACCTATAGAC	2705
Db	2521	CTGGATGGCAAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTTACCTATAGAC	2580
QY	2706	AATTAATGATTTATTTTGGTGTCTGAAGACTACACAGACTGGAGACTTTTTTGGTGAG	2765
Db	2581	AATTAATGATTTATTTTGGTGTCTGAAGACTACACAGACTGGAGACTTTTTTGGTGAG	2640
QY	2766	ATTCGAGGAGCTGTGATGAAACAAATTGCTTAACAATGGGCTCCTTTAAAGAAATTACCTT	2825
Db	2641	ATTCGAGGAGCTGTGATGAAACAAATTGCTTAACAATGGGCTCCTTTAAAGAAATTACCTT	2700
QY	2826	TATGACTTACCAAGCCATATGTTGATAGGCCAACACAAAGAAAGCAGCANTGGCGCCCATGGGCTC	2885
Db	2701	TATGACTTACCAAGCCATATGTTGATAGGCCAACACAAAGAAAGCAGCANTGGCGCCCATGGGCTC	2760
QY	2886	CTGGATCCTTATTAATGCTTCTCTCTGCAAGTAAATGATCATGACAGAACTTGTCTTG	2945
Db	2761	CTGGATCCTTATTAATGCTTCTCTCTCTGCAAGTAAATGATCATGACAGAACTTGTCTTG	2820
QY	2946	TTTCCTGGTGGAAATTTAACCTCTGACAGTTGGTGGCACTCCGAAATGACAGCTAAAGCCAG	3005
Db	2821	TTTCCTGGTGGAAATTTAACCTCTGACAGTTGGTGGCACTCCGAAATGACAGCTAAAGCCAG	2880
QY	3006	AAATTTGAACACACCCCTGGAGCCCTGTGATACGAATATTCACGCAATTCGCTCTGAGCGC	3065
Db	2881	AAATTTGAACACACCCCTGGAGCCCTGTGATACGAATATTCACGCAATTCGCTCTGAGCGC	2940
QY	3066	ACCATCAAGAGACTACAGAGGAATATTGCTTGTGAAGACTGTGCTCAAGTCCCTTTGCATC	3125
Db	2941	ACCATCAAGAGACTACAGAGGAATATTGCTTGTGAAGACTGTGCTCAAGTCCCTTTGCATC	3000
QY	3126	CAGCAAAATCCCAAGACGACACTGTTCAATGTGTGTGGTGGAGACAGCAGCTGCTGTGA	3185
Db	3001	CAGCAAAATCCCAAGACGACACTGTTCAATGTGTGTGGTGGAGACAGCAGCTGCTGTGA	3060
QY	3186	TCTGTGGGCCCCCATACCACTGGCACCCTATGAAATTCAGGTATTAATATCCCTTAAAGTG	3245
Db	3061	TCTGTGGGCCCCCATACCACTGGCACCCTATGAAATTCAGGTATTAATATCCCTTAAAGTG	3120
QY	3246	GAACGCTTAAAGGCCAGAGAATACGAAGAGGCCGCCAGAAATCTTGTATGAGCTTCCATCGC	3305
Db	3121	GAACGCTTAAAGGCCAGAGAATACGAAGAGGCCGCCAGAAATCTTGTATGAGCTTCCATCGC	3180
QY	3306	GAGGAATTCAGAGGAGTGTGGGGGTGGCGGAGTCTTCAAGCCAGCAGTCCCTCTT	3365

Db	3181	GAGGAGAAATGCAGAGGAATGTGGGGGTGGCCGCAAGTCTCCAAAGCCCAAGACAGTCTCCTT	32401
Qy	3366	GTGCTCCCTCTGTCTTTTGATCCTCTTCTCAAGTGA	3401
Db	3241	CTGCTCCCTCTGTCTTTGATGCTCTCTTCAAGGTGA	3276
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; Sequence 3, Application US/09875423			
; Patent No. US20020081657A1			
; GENERAL INFORMATION:			
; APPLICANT: Curtiss, Rory A.J.			
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL			
; TITLE OF INVENTION: FILER, A MEMBER AND USES THEREOF			
; FILE REFERENCE: 10448-059001			
; CURRENT APPLICATION NUMBER: US/09/875,423			
; CURRENT FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: US 60/209,257			
; PRIOR FILING DATE: 2000-06-05			
; NUMBER OF SEQ ID NOS: 6			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 3			
; LENGTH: 3276			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
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Query Match			
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Matches 3257; Conservative 1; Mismatches 0; Indels 18; Gaps			
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Db	1	ATGGCGGGGCGGGGCTGGCGCGCGCGCGCTCCCGGGGGGCGCTCGGCGCTTCGCTGCC	60
Qy	204	GCGCTTCTACGCCGCGCGCTGGGGAGTGTGCGCTCGAGAGCAGCATACCGCTTCC	263
Db	61	GCGCTTCTCTACGCCGCGCGCTGGGGAGTGTGCGCTCGAGAGCAGCATACCGCTTCC	120
Qy	264	GTGGTGAAGCTCTGGGCTCGGCTTTTGGTGGGGAATAAATCCATTGCTCTAAGTAC	323
Db	121	GTGGTGAAGCTCTGGGCTCGGCTTTTGGTGGGGAATAAATCCATTGCTCTAAGTAC	180
Qy	324	TCCGTTCCCAAGCTTTCGCAAAAGAAATACAAAGATATGAGAAAGACGTTCCATAGAA	383
Db	161	TCCGTTCCCAAGCTTTCGCAAAAGAAATACAAAGATATGAGAAAGACGTTCCATAGAA	240
Qy	384	GAAATTGATGGCCCTCCCAACTGTGTAAAGAGCTTGGCAAGACATGGAAGAGATGTTTAC	443
Db	241	GAAATTGATGGCCCTCCCAACTGTGTAAAGAGCTTGGCAAGACATGGAAGAGATGTTTAC	300
Qy	444	AAGAAGTCTGAGGCCGTGAGGCGTCTGTGTGAGGCTGCAGAAAGAACACACCTGAACAT	503
Db	301	AAGAAGTCTGAGGCCGTGAGGCGTCTGTGTGAGGCTGCAGAAAGAACACACCTGAACAT	360
Qy	504	GAAATTGATGAGCACTACAGTATGAAATCTTCAATGCTGTGCTCTATTAATGAAGGAC	563
Db	361	GAAATTGATGAGCACTACAGTATGAAATCTTCAATGCTGTGCTCTATTAATGAAGGAC	420
Qy	564	AAAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATTTAGCCCCAAATGACCATTTT	623
Db	421	AAAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATTTAGCCCCAAATGACCATTTT	480
Qy	624	AATTAATTTGCGTGTGAACATCACTAAGTGAAGTCCAAAGTACCAAGACATGTACAC	683
Db	481	AATTAATTTGCGTGTGAACATCACTAAGTGAAGTCCAAAGTACCAAGACATGTACAC	540
Qy	684	AAAGACCTTCATTTGTCATATGGGGTTTATTTGTGTGATCTCTTAACAAAGTTTTGTA	743
Db	541	AAAGACCTTCATTTGTCATATGGGGTTTATTTGTGTGATCTCTTAACAAAGTTTTGTA	600
Qy	744	GATTAACCTTACCGTGAACCATCTCTCATATGGACATGACTTTGGAAAGTGCAGAAAGGCTTT	803



	11.1%;	Score 419;	DB 10;	Length 519;
Query Match	Similarity 100.0%;	Pred. No. 3.1e-109;		
Matches 419;	conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	688	ACCCGCGCAATTTTCATATGGGGTTATTGTCGTGAATCTCTAAACAAAGTTTGTAGATA	747	
Db	1	ACCCGCGCAATTTTCATATGGGGTTATTGTCGTGAATCTCTAAACAAAGTTTGTAGATA	60	
QY	748	ACTTTGACCGTGACCAATCTCATATGGCGAGTCTTTGGAAGTGCACAAAGCGCTTTT	807	
Db	61	ACTTTGACCGTGACCAATCTCATATGGCGAGTCTTTGGAAGTGCACAAAGCGCTTTT	120	

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? PRIOR FILING DATE: 2001-07-13
? PRIOR APPLICATION NUMBER: US 60/302,277
? PRIOR FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: US 60/298,698
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: US 60/293,574
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 112
? SOFTWARE: JPatent
? SEQ ID NO: 99
? LENGTH: 667
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: 5'UTR
? LOCATION: 1..94
? NAME/KEY: CDS
? LOCATION: 95..613
? NAME/KEY: 3'UTR
? LOCATION: 614..667
? NAME/KEY: polyA_signal
? LOCATION: 636..641
? NAME/KEY: polyA_site
? LOCATION: 652..667
?-S-09-924-340-99

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Query Match	10.3%	Score 387.2	DB 9	Length 667
Best Local Similarity	96.3%	Pred. No. 4.6e-100		
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1508	TTACATTGACAGCACTCTGACTGATGATCAGGGCCCCGTCCTGTATGACCACTTAACCAT	1567		
157	TTTCTCTTCATCCAGCGTGTGATGATCAGGGCCCGTCTGTATGACCACTTAACCAT	216		
1568	GCCTGTGTTTGTAGTAAGCAGAACGAAACCAATGTCGAAAGCATCTTCTGGAGTGGTTGG	1627		
217	GCCTGTGTTTGTAGTAAGCAGAACGAAACCAATGTCGAAAGCATCTTCTGGAGTGGTTGG	276		
1628	CACAGATGTCCCATGAAAGAACTTCTGAAAGACCATCCCAATTAACAAGTTAGGATTTC	1687		



Db 277 CACAGATGTCCAGTGAAGAACTTCTGAGACCATCCCAATATACAGTTAGGGATTCA 336  
OY 1688 CGGTATGCTTTCATCAATAATAGTATATCTGACGCATCCGGACCTGAGCT 1747  
Db 337 CGGTATGCTTTCATCAATAATAGTATATCTGACGCATCCGGACCTGAGCT 396  
OY 1748 GCTGTAGCAAGAGAAAGAAAGCAAGAGAACTATAGTATGCTGACCTCTCTGA 1807  
Db 397 GCTGTAGCAAGAGAAAGAAAGCAAGAGAACTATAGTATGCTGACCTCTCTGA 456  
OY 1808 GCTGTAGTGGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAAATCGAAGACGGG 1867  
Db 457 GCTGTAGTGGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAAATCGAAGACGGG 516  
OY 1868 GAATTTTCCATGAGGTGAAGAGACAGTGCAGAAAGGAGCGGTTT 1917  
Db 517 GAATTTTCCATGAGGTGAAGAGACAGTGCAGAAAGGAGCGGTTT 566

## RESULT 8

US-09-992-600A-99  
; Sequence 99, Application US/09992600A  
; Publication No. US20030027161A1  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US4.DIV  
; CURRENT APPLICATION NUMBER: US/09/992.600A  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 09/924.340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305.456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302.277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298.698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293.574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: Jpatent  
; SEQ ID NO 99  
; LENGTH: 667  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: 1..94  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 95..613  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 614..667  
; FEATURE:  
; NAME/KEY: polyA\_signal  
; LOCATION: 636..641  
; FEATURE:  
; NAME/KEY: polyA\_site  
; LOCATION: 652..667  
US-09-992-600A-99

Query Match 10.3%; Score 387.2; DB 9; Length 667;  
Best Local Similarity 96.3%; Pred. No. 4,6e-100;  
Matches 395; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1508 TTACATGTGACACACTCTACATGATGATAGGCGCCGCTCTGATGACACCTGTAGCCAT 1567  
Db 157 TTTCCTTCATTCAGATGATGATGATGAGGCGCCGCTCTGATGATGACACCTGTAGCCAT 216

OY 1568 GCTGTGTATAGTAAGCAAGCAACACATGTCGAGGCAATTTCTTGGAGTGTGG 1627  
Db 217 GCTGTGTATAGTAAGCAAGCAACACATGTCGAGGCAATTTCTTGGAGTGTGG 276  
OY 1628 CACAGATGTCCAGTGAAGAACTTCTGAAAGACCATCCCAATATACAAATGATGAGATTCA 1687  
Db 277 CACAGATGTCCAGTGAAGAACTTCTGAAAGACCATCCCAATATACAAATGATGAGATTCA 336  
OY 1688 CGGTATGCTTTCATCAATAATAGTATATCTGACGCATCCGGACCTGAGCT 1747  
Db 337 CGGTATGCTTTCATCAATAATAGTATATCTGACGCATCCGGACCTGAGCT 396  
OY 1748 GCTGTAGCAAGAGAAAGAAAGCAAGAGAACTATAGTATGCTGACCTCTCTGA 1807  
Db 397 GCTGTAGCAAGAGAAAGAAAGCAAGAGAACTATAGTATGCTGACCTCTCTGA 456  
OY 1808 GGTGAGTGGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAAATCGAAGACGGG 1867  
Db 457 GGTGAGTGGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAAATCGAAGACGGG 516  
OY 1868 GAATTTTCCATGAGGTGAAGAGACAGTGCAGAAAGGAGCGGTTT 1917  
Db 517 GAATTTTCCATGAGGTGAAGAGACAGTGCAGAAAGGAGCGGTTT 566

## RESULT 9

US-10-116-949-1  
; Sequence 1, Application US/10116949  
; Publication No. US20030044911A1  
; GENERAL INFORMATION:  
; APPLICANT: Lerman, Michael I.  
; APPLICANT: Minna, John D.  
; APPLICANT: Latif, Farida  
; APPLICANT: Wei, Ming-Hui  
; APPLICANT: Sekido, Yoshitaka  
; APPLICANT: Gao, Boning  
; APPLICANT: Duh, Fuh-Mei  
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof  
; FILE REFERENCE: NIH-05043  
; CURRENT APPLICATION NUMBER: US/10/116.949  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470.443  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 5463  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (162)..(3599)  
US-10-116-949-1

Query Match 5.7%; Score 214; DB 9; Length 5463;  
Best Local Similarity 47.3%; Pred. No. 6.9e-50;  
Matches 845; Conservative 0; Mismatches 900; Indels 41; Gaps 5;

OY 61 GGGCTGCGCCACCGCCGCTCCGCGAGCTCCCGGCGGCGCTCTGTCGTCGCGCGCAC 120  
Db 165 GCGGTGCGCGCTCGGACCTGCGGCGCTCTCGGCGCGCGCGCGCGCGCTCGCGCGCC 224  
OY 121 GGGCGCTGCGAGAGAGCCAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180  
Db 225 TGGCGCGCTGCGGCG 284  
OY 181 GGGCGCTGCGGCTCTGCTGCGCGCGCGCTCTGACCGCGCGCGCGCGCGCGCGCT 240  
Db 285 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344  
OY 241 CGGACGACGAGATACCGCTCTCGGTGAGAGCTCTGGGCGCTTTTGGTGGGAGAGA 300

Db 345 TACAGCTTC - CCCCACAGCAGCAGATGACGACTGGGCCCGCGCTCGAGAGCAGAGG 402  
 QY 301 TAAATTCATTCGCTGTAAGTACTCCGTTCCAGCTTTCGCAAAAGAAATACAAAGT 360  
 Db 403 TCGAGCGCGTGAATGCGGATTTTGGAGCGCTCCAGCAGCTCGTGAAGATTCACAGACA 462  
 QY 361 ATGAGAAAGAGCTTCCATAGAAATTTGATGGCTCCAACTGGTAA/AGAGCTGGCAA 420  
 Db 463 ACCGGAACCTGTGAGTGCAGAGAGAAATGAGCCTCAGAAAGTTGGTGGAGAGTGGCAG 522  
 QY 421 AGAATATGAGAGATGTTTCAACAAGATCTGAGCGCTGAGCGCTGTGGTGGAGCTG 480  
 Db 523 GGGACATTTGAGACCTTCTGAGAGAGAGTGGAGCGCTGGAAGAGACTGGCTGATCTG 582  
 QY 481 CAGAAAGACACACCTGAAACATGAAATTTGATGACAGCTACGATAGTACTT----- 535  
 Db 583 CAGAGAACTTCCAGAAAGCAGCCGCTGGCAGACACATCAAGAGAGAGACATCGTGT 642  
 QY 536 -----CAATGCTGTGCTGATTAATGAAAGGAGCAAGAGCGGAAAT 576  
 Db 643 ACTATGACGCCAAGGCTGACGCTGAGCTGAGACCCCTGAGATGAGATGTGGAAAGG 702  
 QY 577 TTTTGAAGCTGGGAAAGAAATTCATCTTACCCCAATGACCATTTTAAATTTGGCTG 636  
 Db 703 GGTCTAAGGCCAGCACCCTAAGGCTGACTTATCGAGAGCCCAACCTTCAAGAACAG 762  
 QY 637 TGAACATCAAGTCAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 696  
 Db 763 TCAACTATTCATACGCGGCTGTACAGATCCCTAAGGACATCTCAAAAGCTCCACGTCA 822  
 QY 697 TGTCAATGGGGTTTATGCTGTAATCTCTAACAAGTTTGTGATTAATCTTGAC 756  
 Db 823 TCCCTCAATGAGCTCAACTGACAGAGAGCCCTGAGAAATGTTCATGAGAAACCGAGAC 882  
 QY 757 GTGACCCATCTCTCATATGCGCAGTACTTGGAAAGTGCAGAAAGGCTTTTAAAGCAGTATC 816  
 Db 883 AAGACCCCACTGTGTGTGGAGTCTTTCGGCAGCGCCAGAGAGTCACTCGCTACTAC 942  
 QY 817 CGGGATTTAAATGGGAAACAGATGAAATGAGTCACTTCCCTTCGACTCAGAGACCGAA 876  
 Db 943 CGGCCACCCCGTGGGAGAGCCCAAGAAATGACCTGTACATGTCGCAAGGA--GAC 999  
 QY 877 AATGTACATCCAGGAGCAGTCTTCCGAAGAGTGTGATTTTAAATGAGTGTG 936  
 Db 1000 CTTGGTATATCCAGGGGCTGTGACCCCAAGAGATGTCTCATCTGATGATG 1059  
 QY 937 GCAGATGAAGAGTCCGCTGACTATGCGAGCAACACATCTCATTCATTTGGATA 996  
 Db 1060 GCAGTGTAGCGGCTGACCCCTGAGCTGATGAGACATCTGTGCGCAATGCTGGACA 1119  
 QY 997 CACTTGGGAGTATGACTTCTTCAACATTAATGCTTAAATGAGAGCTTCACTATGTTGG 1056  
 Db 1120 CGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1179  
 QY 1057 AACCTTGGCTGAATGAACTTGTGTGCAAGCGAGCAGAGCAAAAGAAAGAAAGAAAG 1116  
 Db 1180 CATGCTTCAACACC-----TGGTGAAGGCCAATGTGCGCAAGAAAGGTGTTCAAGG 1233  
 QY 1117 AGCATCTGACAAACTTTTGGCCAAAGAAATTTGAATGTTGATTTGATGATGAGG 1176  
 Db 1234 AAGCTGTGACAGGATGTTGGCCAAAGGACCAAGGCTTACAGGCGGGTTTGATGATG 1293  
 QY 1177 CCTTCAACATTTGATGATGATTTCAACACAGGAGCAAGAAAGTATCTGAGTCAAGGCCA 1236  
 Db 1294 CTTTGAACAGCTGAGAGATCCAAACATCACTCGGGCC-----AAGTGAAACAAAGATGA 1347  
 QY 1237 TCATGCTCATTAAGTATGAGGCGGTGACACCTATGATATACATCTTTTCAAAATACATTT 1296  
 Db 1348 TCATGATGTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1407  
 QY 1297 GGCAGATTCAGAAAGTGTGCTTTCATATACATCTTGAAGAGAGAGCCGCTTTGAG 1356

Db 1408 GGCCAACCCGAGCGGTGGCGCTTTACTTCTCCGTGGGACATTAATCATCTCA 1467  
 QY 1357 ACAATCTAAAGTGAATGCGCTGTGCAACAAAGATTTTACCAGATTCACCTTGG 1416  
 Db 1468 CACCGCTGAGTGTGATGCGCTGTGCAACAAAGCTACTATTTTGAATGCCCTTCATG 1527  
 QY 1417 CTGATGTGACAGGAAATGTATGATATCTTACGCTGCTTACGCGGCCCAAGTCAATG 1476  
 Db 1528 GAGCATTCGCCATCAACACAGAGAAATATGATGATGATGATGATGATGATGATG 1587  
 QY 1477 ACCAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1536  
 Db 1588 CAGGCAAGAGGAGGCCAAGCAGATGATGATGATGATGATGATGATGATGATGATG 1647  
 QY 1537 AGGGCCCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1596  
 Db 1648 GGTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1707  
 QY 1597 GATCGAAGGCGATTTCTGTGGAGTGTGGACATGTCACATGTCACATGATGATGATG 1656  
 Db 1708 AGAAGAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1767  
 QY 1657 AGACCATCCCAATACAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1716  
 Db 1768 GGTGACCCCAACTACACCTTGGAGCCCAAGGCTATGATGATGATGATGATGATGATG 1827  
 QY 1717 GRTATATCTGACGATCCGGAATCAGGCTGTGATGATGATGATGATGATGATGATGATG 1776  
 Db 1828 GCTAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1887  
 QY 1777 AACCTACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1822  
 Db 1888 CTCTGAGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1933  
 RESULT 10  
 US-10-116-949-3  
 : Sequence 3, Application US/10116949  
 : Publication NO. US20030044911A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Ierman, Michael I.  
 : APPLICANT: Minna, John D.  
 : APPLICANT: Latif, Farida  
 : APPLICANT: Wei, Ming-Hui  
 : APPLICANT: Sekido, Yoshitaka  
 : APPLICANT: Gao, Boning  
 : APPLICANT: Duh, Fuh-Mei  
 : TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof  
 : FILE REFERENCE: NIH-05043  
 : CURRENT APPLICATION NUMBER: US/10/116,949  
 : PRIOR FILING DATE: 2002-04-05  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443  
 : PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22  
 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359  
 : NUMBER OF SEQ ID NOS: 114  
 : SOFTWARE: Patent In Ver. 2.0  
 : SEQ ID NO 3  
 : LENGTH: 5482  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: (181)..(3618)  
 : US-10-116-949-3  
 Query Match 5.7%; Score 214; DB 9; Length 5482;  
 Best Local Similarity 47.3%; Pred. No. 6.9e-50;  
 Matches 845; Conservative 0; Mismatches 900; Indels 41; Gaps 5;

Oy	121	GGGCGGCTGGAGGGAGGCCAAGATGGCCGGGCGGGCTGGCCGCGCGCTCCCGG	180
Db	244	TGGCCCGGCTGGGGCCCGCCACCCTGGCCCCGGCACCCGGCGCCGAGCTCCGGCCCCG	303
Oy	181	GGGCGCTGGCGCTTCGCTGGCGCGCTTCCTACGGCGCGCTGGGGAGCTGGTGGCT	240
Db	304	CGCCCGCTTGCGCTGCTGCTGGCGCTTCCTACCGCTGCTGGCGGCCCGCGCGCTCGCC	363
Oy	241	CGGACGACAGATACCCTCTCCGCGGTGAAGCTCTGGGCTCGGCTTTTGGTGGGAGA	300
Db	364	TACAGCTTC--CCCGAGAGACAGAGATGACGACATGGGCGCGCGCTGTGAGCAGAGAG	421
Oy	301	TAAATTCATTGCTGCTAGTACTCCGGTTCCAGCTTCCTGCAAAAGAAATACAAGAGT	360
Db	422	TGGAGGGGTGATGGGATTTTGGAGGCGCTGCAGACACTCCGAGATTTACAAAGACA	481
Oy	361	ATGACAAGAGCTTGCCATACAGAAATGATGGCTCCCACTGGTAAAGAGCTGGCAA	420
Db	482	ACCGGACCTGTTCCAGGTACAGAGATGAGCTTCAGAAATTGGTGGAAAGCTGGCAG	541
Oy	421	AGCAATGGAGAGATGTTTACAAAGATGTCGAGGCGTACGCGCTGTGGAGGCTG	480
Db	542	GGGACATTGAGAGCTTGTGGACAGAAAGTGGCAGGCGCTGAAAGAGACTGGCTGATGCTG	601
Oy	481	CAGAAGAGCACACCTGAAACATGAAATTTGATGCAGACTTACAGTATGATTACTT	535
Db	602	CAGAGAACTTCAGAAAGACACCGCTGGCGAGCACAATCAAGAGGAAGACATCTGTG	661
Oy	536	-----CAATCTGTGCTGATTAATGAAGGAGCAAGAGCGGAATT	576
Db	662	ACTATGACGCCAGGCTGTACGCTGACGTGGAGCAGACCTGTGAGTGTGAGTGGAAAGG	721
Oy	577	TTTTGGAGCTGGGAAGGAATTCATCTTTAGGCCCAATGACCAATTTTAATATTGGCTG	636
Db	722	GGCTTAAGGCCAGCACCTTAAGGCTGGACTTATCGAGAGAGCCCAAACTTCMAAGACAG	781
Oy	637	TGAACATCAGTCTAAGTACGCTCCAACTACCAAGCAATGTACAACAAGACCGTCGA	696
Db	782	TCAACTATTTCATACGCGGCTGTACAGATCCCTACGCACTCTCAAAAGCTCCACTGTCA	841
Oy	697	TTGTCAATGGGGTTTATTTGGCTCAATCTCTAAAACAAAGTTTTGGAGTAATCTTTGACC	756
Db	842	TCTCTAATGAGACTCACTGAGCAGAGAGCCCTGGAGATGTGTTCATGAGAAACCGCAGAC	901
Oy	757	GTAGCCCATCTCTCATATGGCAGTACTTTTGGAAAGTGCAAAAGGCTTTTGTAGCGATAC	816
Db	902	AAGACCCCACTCTGCTGGAGGCTTTCGGCAGCGCACAGGAGTCACTCGCTACTACC	961
Oy	817	CGGGATTTAATTTGGGAACCAATGAGATGAGATCTATGCTTCGACCTCAGAGAACCGA	876
Db	962	CGGGCACCCGCTGGCGAGCCCCCAAGAAATGCACTGTACGATGTCACCAAGGA--GAC	1018
Oy	877	AATGCTATCATCCAGCAGCAAACTTCTCCGAAGACGTGGCTATTTAGTGTGACGTCAAG	936
Db	1019	CCTGGTATATCCAGGGGGCCGTGCACACCCAAACATGCTCATCTCGATGTGTGAGTG	1078
Oy	937	GCAGCATGAAAGAGACTCCGCTGTGACTATGCGCAGACAAACAGTCTTCATCAATTTTGATA	996
Db	1079	GCACTGTGAGCGGCTCAACCTCAGCTGATGAAGACATCTGCTCCGAGATGTGAGACA	1138
Oy	997	CACATGGGATGATGACTTCTTCACACTAATGCTTATATAGAGAGCTTCACTATGTGG	1056
Db	1139	CGCTGTCTGATGATGACTTATGTGAATGTGGCTTCGTTCAACGAGAAAGCAGCGCTGTGT	1198
Oy	1057	AACCTTGCTGAATGAACTTTGGTGCAGAGCCGACAGCAACAAAGACACTTCAAGG	1116
Db	1199	CATGCTTACACACAC-----TGTGTGAGGCCAATGTGGGCAACAAGAAAGTGTTCAGG	1253
Oy	1117	AGCATCTGCAAAACTTTTGGCCAAAGGAATTTGGAATGTTGGATTAAGCTCTGAATGAGG	1176
Db	1253	AAGCTGTGCAGGGCGATGTGTGGCCAAAGGCCACACAGGCTTACAGGCGCGGCTTTGAGTGTG	1312

Oy	1177	CTTCAACATCTCTGAGATTCTTAAACACACGGCAACAAGATGTCAGATCAGGCCA	1236
Db	1313	CTTTTGACACAGCTCAGAACTCCAACTCACTCTGGGCC-----AACTGCACACAGATGA	1366
Oy	1237	TCATGCTTCATTAAGATGAGGGGCGGTGACACCTATGATACAATCTTTGCCAAATTAACAATT	1296
Db	1367	TCATGATGTTTCACGAGTGGTGGTGAAGGACCGCGTCGAGGACGCTTTTGAGAAGTACAAATT	1426
Oy	1297	GGCCAGATCCAAAGGTTCCGATCTTCACTACTCTTGGACAGAAAGGCTGCGTTTTCG	1356
Db	1427	GGCCAAACCCGAGCGCTGCGGCTTTTACTTTTCTCCGTGGGAGGACATAACTATGACGCA	1486
Oy	1357	ACAATCTAAAGTGATGGCCCTGTGCCACAAGAGATTTTTCACGAGATCTCCACCTTGG	1416
Db	1487	CACGCGTCGACGTGATGGCCTGTGGCCACAAGAGCTACTATTTTGATATCCCTTCATCG	1546
Oy	1417	CTGATGTGCAGAGAAATGTCAATGAAATACCTTCAGCTGCTTACGCCGCCCAAAATCATCG	1476
Db	1547	GAGCATATCCGCATCAACACACAGAAATATCTAGATGTGGTGGCGGCCCATGTGCTGG	1606
Oy	1477	ACGAGAGCATGATGATGGTGTGGACCGAAGCTTACATTGACAGCAGCTTGACTGATATC	1536
Db	1607	CAGGCAAGGAGGCCAACAGCAAGTTCACTGACACCACTGTATGAGGATCACTGGGACTCG	1666
Oy	1537	AGGGCCCCGCTCGATGAGCACCACTGTAGCCATCGCTGTGTTTAAAGCAGAACCAACA	1596
Db	1667	GGTTGTGTGTAAACAGGAGCCCTCCCTGTTTTCACCTGCACAGAGATGGCCCTGGGGAA	1726
Oy	1597	GATCGAAGGCGATCTTCTTGGGAGATGGTGGCACAAGATGTCCCACTGAAACAACTTCTGA	1656
Db	1727	AGAGAACAACGCTGATCTGGGGGTGATGGGATTTGACGTGGCTGCTGTGATTAACATCAAGA	1786
Oy	1657	AGACATATCCCAATTAACAAGTTAGAGGATTCACAGTTATGACCTTTGCATCAACAATATATG	1716
Db	1787	GGGTACGCCCACTACAGCTGTGAGGCCAACAGCGCTATGTGTTCCTTACCTGAAAGC	1846
Oy	1717	GRTATATCTGACGCACTCCGGAATTCAGGCTGCTGTACGAAGAAAGAAAAGGAAGA	1776
Db	1847	GCTACGTGTGTGACACCCCAATCTTCACAGCCCAACACCACTTCGCGGAGCGCTTGA	1906
Oy	1777	AACCTACTATATAGCGTTGAGACCTCTCTGAGATGGAGATGGGAAGA	1822
Db	1907	CTCTGGACTTCTCGATGCGGAGCTTGAAGATGAACAACAGAAAGA	1952

RESULT 11  
 US-10-116-949-5  
 Sequence 5, Application US/10116949  
 Publication No. US20030044911A1  
 GENERAL INFORMATION:  
 APPLICANT: Lerman, Michael I.  
 APPLICANT: Minna, John D.  
 APPLICANT: Latif, Farida  
 APPLICANT: Wei, Ming-Hui  
 APPLICANT: Sekido, Yoshitaka  
 APPLICANT: Gao, Boning  
 APPLICANT: Duh, Fuh-Mei  
 TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof  
 FILE REFERENCE: NIH-05043  
 CURRENT APPLICATION NUMBER: US/10/116,949  
 CURRENT FILING DATE: 2002-04-05  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443  
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359  
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30  
 NUMBER OF SEQ ID NOS: 114  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 5279  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS



```

RESULT 14
US-10-090-827-11
; Sequence 11, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:

```

Query Match	3.5%	Score 130.6	DB 9	Length 3109
Best Local Similarity	46.4%	Pred. No. 3.4e-26		
Matches 673	Conservative	0	Mismatches 739	Indels 39
				Gaps 6

Db. 950 TGTGTAAGAGACGGCGTGAATATATATCAACGCCAAAGGAATTACAGATTATATAAGAAGGGCT 1009  
QY 1168 TGATGAGGCCTTCAACTTTTGATGTGATTTTCACACACGGGACACAGAAAGTATCTCA 1227  
Db 1010 TTATGTTTTGCTTTTGAACAGCTGCTTATATTTAATGTTTTCCAGAGCA-----AACTCCA 1063  
QY 1228 GTCAGGCCATCATGCTCATAACTGATGGGGGGGTGGACACCTATGATATCAATCTTTGCAA 1287  
Db 1064 ATTAGATTATTTATGCTTTTCAGGGATGAGAGAGAAGAGAGCCAGAGATATTTAACCA 1123  
QY 1288 AATATCAATTGGCCAGATGCAAGAGTGTGCATCTTTCACATPACCTCATTGGAGAGAGCGTG 1347  
Db 1124 AAATACAAT---AAAAGATAAAAAAGATAGCTGATTCAGGTTTTTCAGTTGTCACACAAATT 1180  
QY 1348 CGTTTGACAGCAATCTPAAGAGGATGAGCGTGGCCATGGCCAAAGATTTTACCAGATCT 1407  
Db 1181 ATGAGAGAGACCTATTTCAGTGGAGTGGCTGTGAAACAAAGGTATATTATTAATAATTC 1240  
QY 1408 CCACCTTGAGCTGATGTGACAGAGAAATGTCATGTAAATACCTTCACGTGCTTAGCCGCCCA 1467  
Db 1241 CTTCATTTGGTGCATATTAAGATCAATCTCAGAAATTTTGGATGTTTTGGGAAGACCAA 1300  
QY 1468 AATTCAT-----CGACCAGAGCATATGTGTGTGGACCGAAGCTTACATTACACAGA 1521  
Db 1301 TGGTTTTAGCAGAGACAAAGCTTAAGCAAGTCCCAATGCAAAATGTACTCGATGCAT 1360  
QY 1522 CTGTGACTGATGTATGATCAAGGGCCCCGCTCTGTATGATCACTAGACCATGCTGTGTTACTA 1581  
Db 1361 TGGAACTGGACCTTGTCATTACTTGAACCTTTCCGGTCTTCAACATPAACGGCCAAATTTG 1420  
QY 1582 AGCAGAACGAAACACAGATCGAAGGGCAATCTCTTGGAGATGGTGGCACAGATGTCCAG 1641  
Db 1421 AAAATTAAGACAAACTTAAGAACACAGCTGATGTTCTGGTGTGATGGAGTATGATGTCTT 1480  
QY 1642 TGAAGAAACTTCTGAGAGACCATCCCAGAAATACAGATTAGGATTCACGGTTATGCTTTG 1701  
Db 1481 TGSAAATATTTAAAGACTGACACACAGTTTTTACACTGTGCCCCAAATGGGTATTACTTTG 1540  
QY 1702 CAATCAAAATATGRTATATCTTACAGCATCCGGAATCCAGAGCTCTGTACGAMAGAG 1761  
Db 1541 CAATGATCTTATGTTATGTTTATTTATCATCCAAATCTTCAGCCAAAGACCCCAAT 1600  
QY 1762 GAATAAAGCGCA 1772  
Db 1601 CTCAGAGACCA 1611

RESULT 15  
US-10-090-827-12  
; Sequence 12, Application US/10090827  
; Publication No. US20030073132A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert  
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subunit  
; TITLE OF INVENTION: binding ligands  
; FILE REFERENCE: 179  
; CURRENT APPLICATION NUMBER: US/10/090,827  
; CURRENT FILING DATE: 2002-03-06  
; PRIOR APPLICATION NUMBER: US/09/397,549  
; PRIOR FILING DATE: 1999-09-16  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 3190  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-090-827-12

Query Match 3.5%, Score 130.6, DB 9, Length 3190;  
Best Local Similarity 46.4%; Pred. No. 3,4e-26;  
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 AGAATATCAAGAGTATGAGAAAGACGTTGCCATAGAGAAATTTGATGGCCCTCCAACTGG 405  
 Db 176 ATATTATGAGAAATATCAAGATTTGTATAGTGTGAGAACCAAAATATATGACAGCCAGCTGG 235  
 QY 406 TAAAGAGCTGGCAAGAACATGAGAGATGTTTACAGAACTGTGAGCCCTCAGGC 465  
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 QY 1408 CCAGCTTGGCTGATGTGACGAGAAATGTCATGAAATACCTTCACGCTGTTAGCCGCGCA 1467

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 QY 1642 TGAAGAACTTCTGAGAACCATCCCAAAATCAAGTTAGGATTTACGGTTATGCTTTG 1701  
 Db 1481 TCGAAGATATTAAGAAAGACTGACACAGCTTTTACATGCTGCCCCAATGGGATTAATCTTG 1540  
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 Job time : 429 secs



GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2003, 21:24:01 ; Search time 201 Seconds

(without alignments)  
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Title: US-09-787-657-3

Perfect score: 3770

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	5.7	5463	US-09-470-443-1	Sequence 1, Appl
2	214	5.7	5482	US-09-470-443-3	Sequence 3, Appl
3	206.4	5.5	5279	US-09-470-443-5	Sequence 5, Appl
4	130.6	3.5	3566	US-07-745-206A-24	Sequence 24, Appl
5	130.6	3.5	3566	US-08-311-363-24	Sequence 36, Appl
6	130.6	3.5	3579	US-08-455-543A-35	Sequence 35, Appl
7	130.6	3.5	3579	US-08-193-078B-25	Sequence 25, Appl
8	130.6	3.5	3579	US-08-223-305C-36	Sequence 36, Appl
9	130.6	3.5	3579	US-08-949-386-32	Sequence 32, Appl
10	130.6	3.5	3579	US-08-450-562-32	Sequence 32, Appl
11	130.6	3.5	3579	US-08-984-709A-32	Sequence 32, Appl
12	130.6	3.5	3579	US-08-450-272-32	Sequence 32, Appl
13	130.6	3.5	3600	US-08-455-543A-11	Sequence 11, Appl
14	130.6	3.5	3600	US-08-455-543A-33	Sequence 33, Appl
15	130.6	3.5	3600	US-08-193-078B-11	Sequence 11, Appl
16	130.6	3.5	3600	US-08-223-305C-11	Sequence 11, Appl
17	130.6	3.5	3600	US-08-223-305C-33	Sequence 33, Appl
18	130.6	3.5	3600	US-08-149-097D-11	Sequence 11, Appl
19	130.6	3.5	3600	US-08-949-386-11	Sequence 11, Appl
20	130.6	3.5	3600	US-08-450-562-11	Sequence 11, Appl
21	130.6	3.5	3600	US-08-984-709A-11	Sequence 11, Appl
22	130.6	3.5	3600	US-08-450-272-11	Sequence 11, Appl
23	130.2	3.5	3564	US-08-455-543A-35	Sequence 35, Appl
24	130.2	3.5	3564	US-08-193-078B-24	Sequence 24, Appl
25	130.2	3.5	3564	US-08-223-305C-35	Sequence 35, Appl
26	130.2	3.5	3564	US-08-949-386-31	Sequence 31, Appl
27	130.2	3.5	3564	US-08-450-562-31	Sequence 31, Appl

28	130.2	3.5	3564	US-08-984-709A-31	Sequence 31, Appl
29	130.2	3.5	3564	US-08-450-272-31	Sequence 31, Appl
30	130.2	3.5	3565	US-08-455-543A-34	Sequence 34, Appl
31	130.2	3.5	3585	US-08-193-078B-23	Sequence 23, Appl
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36	130.2	3.5	3585	US-08-450-272-30	Sequence 30, Appl
37	130.2	3.5	3636	US-08-455-543A-32	Sequence 32, Appl
38	130.2	3.5	3636	US-08-193-078B-22	Sequence 22, Appl
39	130.2	3.5	3636	US-08-223-305C-32	Sequence 32, Appl
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41	130.2	3.5	3636	US-08-450-562-29	Sequence 29, Appl
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43	130.2	3.5	3636	US-08-450-272-29	Sequence 29, Appl
44	130.2	3.5	3657	US-08-455-543A-20	Sequence 20, Appl
45	130.2	3.5	3657	US-08-223-305C-20	Sequence 20, Appl

## ALIGNMENTS

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RESULT 1
US-09-470-443-1
; Sequence 1, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boqing
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; EARLIER FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(3599)
US-09-470-443-1
Query Match
Best Local Similarity 47.3%; Pred. No. 8e-42;
Matches 845; Conservative 0; Mismatches 900; Indels 41; Gaps 5;
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DB	285	CGCCCGCTGGGAGGAGCCACGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	344
QY	241	CGGACGACGATGACGCTTCGCTGCTGAGCTTCGCGCGCGCGCGCGCGCGCG	300
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[illegible]

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Db	1607	CAGGAAGAGGCGCAACACAGCTTCATGGAGCAACCTGTATAGGATGCACCTGGGACTCG	1666
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Qy	1597	GATCGAAGGGGATTCCTCTGCGGAGTGGTGGACAGATGTCCTCCATGGAAGAAACTTCTGA	1656
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Qy	1777	AACCTACTATAGTAGCGTTGAGCTCTCTGAGGTGGAGTGGGAAGA	1822
Db	1907	CTCTGGAGCTCTCGATGCGGAGACTATGAGATGAGAAACAGAGMAA	1952

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RESULT 3
US-09-470-443-5
Sequence 5, Application US/09470443
Patent No. 6441156
GENERAL INFORMATION:
APPLICANT: Ierman, Michael I.
APPLICANT: Minna, John D.
APPLICANT: Latif, Farida
APPLICANT: Wei, Ming-Hui
APPLICANT: Sekido, Yoshitaka
APPLICANT: Gao, Boning
APPLICANT: Du, Fuh-Mei
TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
FILE REFERENCE: NIH-05043
CURRENT APPLICATION NUMBER: US/09/470,443
CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 60/114,359
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 5279
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (185)..(3415)
US-09-470-443-5

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Query Match	5.5%	Score 206.4	DB 4	Length 5279
Best Local Similarity	47.9%	Pred. No. 5.3e-40		
Matches 757	Conservative	0	Mismatches 786	Indels 39
				Gaps 4
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STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3273  
US-07-745-206A-24

Query Match 3.5%; Score 130.6; DB 1; Length 3566;  
Best Local Similarity 46.4%; Pred. No. 22;  
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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1361 TGAAGTGGGACTTGTATTTACTGGAACCTTCCGCTTCAACATTAACCGGCAATTTG 1420  
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1762 GAAAAAGGA 1772  
1601 CTCAGAGCCA 1611

RESULT 5  
US-08-311-363-24  
Sequence 24, Application US/08311363  
Patent No. 5876958  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311.363  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745.206  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-51506  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3566 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..3273  
 US-08-311-363-24

Query Match 3.5% Score 130.6; DB 2; Length 3566;  
 Best Local Similarity 46.4%; Pred. No. 8e-22;  
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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 DB 716 GCAGAGACCAATGGTACATCCAAAGAGCTGATCTTAAAGACATGCTTATTTGTTGG 775  
 QY 928 ACCTGAGTGGCAGATGAAGAGACTCCGCTGACTATGCGGAGCAACACATCTTCATCA 987  
 DB 776 ATGTGAGTGAAGTGTATGATGATTTGACACTTAACTGATCCGAACATCTCTCCGAAA 835  
 QY 988 TTTTGGATACACTTGGGAGTATGACTTTTCAACATTAATTTATTAAGAGAGCTTC 1047  
 DB 836 TGTTAGAAACCTCTCAATGATGATTTTGTGAATGATGCTTCAATTTAAGCAGCATGCTC 895  
 QY 1048 ACTATGTGAACCTTGGCTGAATGAAGACTTTGGTCAAGCCGACAGCAAAAGAGAGC 1107  
 DB 896 AGCATGTAACTGTTTTCAGCACC-----TTGTCCAAAGCAAAATGTAAGAAATAAAG 949

QY 1108 ACTTCAGGAGACATCTGACAACTTTTCCGCAAGAAATTTGATGATTTATACCTC 1167  
 DB 950 TGTGAAAGACGCGGTGAATTAATATACAGCCAAAGAAATTAAGATTAAGAGGCT 1009  
 QY 1168 TGAATGAGGCTTCAACATTTTGTAGTATTTCAACACACGCGGACAAAGAAATTTGCA 1227  
 DB 1010 TTAGTTTGTCTTTGAAACAGCTGCTTAATTAATGTTTCCAGAGCA-----AACTGCA 1063  
 QY 1228 GTCAAGCATCATCTCTAATACATGATGAGGCGGTGAGACACTATGATTAACATCTTGC 1287  
 DB 1064 ATAGATTAATTAATCTTTTACAGATGAGAGAGAGAGAGCCAGAGATTAATTAACA 1123  
 QY 1288 AATTAATTTGGCCAGATGAAAGGTTGCACTTTCACATCTCATTTGAGAGAGAGCTG 1347  
 DB 1124 AATCAAT-----AAAGATTAATAAGTACGTGATTCAGTTTTCAGTTGGTCAACACAT 1180  
 QY 1348 CGTTTGCAGACATCTTAATGATGATGCTGTGCTGCAACAAAGATTTTAAACCAATCT 1407  
 DB 1181 ATGAGAGAGACCTTATTCAGTGTGATGCTGTAACAAAGCTTATTAATTAAGAAATTC 1240  
 QY 1408 CCACTTGGCTGATGTCAGAGATGTCATGGAATPACCTTCAAGTCTTAAGCGGCCCA 1467  
 DB 1241 CTTCATTTGTCGATTAAGATCAATTAATCAATTAATTTGATGTTTGGAGAGACCAA 1300  
 QY 1468 AAGTCAAT-----CGACGAGACATGATGTTGTTGAGACGGAAGCTTACATTTGACAGCA 1521  
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 QY 1522 CTCTGACTGATGATCAAGGCGCCGCTGCTGATGACCACTGTAGCCATGCTGTTAGTA 1581  
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 QY 1582 AGCAGACGAAACCAATGGAAGGCAATCTTGTGAGAGTGTGACAGATGCTCCAG 1641  
 DB 1421 AAATTAAGCAAACTTAAGAAACCACTGATTTTGTGTGATGAGAGATGTTCTTT 1480  
 QY 1642 TGAAGACTTCTGAAGACCAATCCCAAAATACAAAGTTAGGATTCAGGTTTATGCTTTG 1701  
 DB 1481 TGAAGATTAATTAAGAGTACGACACGTTTACATGATGAGCCCAATGATTTACTTTG 1540  
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 DB 1541 CAATGATCTTAATGATTTATTTTATTAATCAATCAATCTCAGCAAAAGACCCCAAT 1600  
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 DB 1601 CTCAGAGGCA 1611

RESULT 6  
 US-08-455-543A-36  
 : Sequence 36, Application US/08455543A  
 : Patent No. 5792846

GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE:  
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 FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 35...3289  
 OTHER INFORMATION: Standard name "alpha2"  
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 NAME/KEY: 3'UTR  
 LOCATION: 3290...3579  
 OTHER INFORMATION:  
 US-08-455-543A-36

Query Match 3.5% Score 130.6; DB 1; Length 3579;  
 Best Local Similarity 46.4%; Pred. No. 8e-22;  
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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 QY 406 TAAAGAACTGGCAAGAAATGAGAGATGTTTCCAGAAAGTCTGA3GCCGTCAGGC 465  
 DB 270 TAGAAATTCAGCCGAGATATTTGGAACACTTCTAGCAACAGATCTTAAGCCCTGGTGA 329  
 QY 466 GTCG-----GTGAGGCTGCGAAGAACACACCTGAAACATGANTTTGATGAG 516

DB 330 GCCTGCATTGGAAGCGAAGATTCAACGACCTCACAGTGAGAGAGATTTTGCA 389  
 QY 517 ACTTACAGTATGTAATCTTCAATGCTGTGTATTAATGAAGGACAAAGAGGGAATT 576  
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 DB 750 GCAGAGACCATGCTACATCAAGAGCTGCACTCTTAAGACATGCTTATCTGTGG 809  
 QY 928 ACCTGAGTGCAGCATGAAGAGACCTCCGCTGACTATTCGGAAGCAAGACGTCATCA 987  
 DB 810 ATGTGATGGAAGTGTATGATGATGACACTTAAGTATCCGACATGCTGTCGAAA 869  
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 QY 1048 ACTATGTGAACTTGGCTGTAATGAGACTTTGGTGCAGCCGACAGACAAACAAAGACC 1107  
 DB 930 AGATGTAGCTGTTTTCAGCACCC-----TTGTCCAAACCAATGTAAGAAATTAAG 983  
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 DB 1215 ATGAGAGAGAGACTATTCAGTGTGATGCTGTGAAAACAAAGSTTTATTTATGAATTC 1274  
 QY 1408 CCACCTTGGCTGATGTGACGAGAAATGTCATGAATATCTTACGTCCTTTACCGGCCCA 1467  
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 QY 1522 CTCTACATGATGATGAGGCGCCCTGCTGATGACCATGTTACCATGCTGTTAGTA 1581



Db 1395 TGGAACTGGAGCTGTGCTATTACTGGAACTCTCCGCTCTTCAACATACCGGCAATTGG 1454  
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Db 1575 CAATGATCTTAATGGTATTGTTTATTACATCCAAATCTTCAGCAAAAGAACCCCAAT 1634  
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Db 1635 CTCAGAGCCA 1645

RESULT 7  
US-08-193-078b-25  
Sequence 25, Application US/08193078B  
Patent No. 5846757  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN  
STREET: 1660 UNION STREET  
CITY: SAN DIEGO  
STATE: CA  
COUNTRY: USA  
ZIP: 92101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/193,078B  
FILING DATE: 07-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/868,354  
FILING DATE: 10-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seldman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-53607  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
NAME/KEY: CDS  
LOCATION: 35..3289  
OTHER INFORMATION: /standard\_name="Alpha-2e"

FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..34  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 3289..3579  
US-08-193-078b-25

Query Match 3.5%; Score 130.6; DB 2; Length 3579;  
Best Local Similarity 46.4%; Pred. No. 8e-22;  
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 AGAATACAAAGACTATGAGAAAGACGTGGCATAGAGAAGAAATGATGGCTCCCACTGG 405  
Db 210 ATATTATGAGAAATATCAAGATTGTATACGTGGAACCAAAATATGACACCGCAGCTGG 269  
QY 406 TAAAGAGCTGGCAAGAACATGGAAGAGATGTTTCAACAAAGCTGAGGCGCTCAGGC 465  
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QY 466 GTCGTG-----GTGAGAGCTGCAGAGAGACACCTGAAACATGATTTGATGACAG 516  
Db 330 GCTTGGCATTTGAAAGCGGAGAAAGTTCAACAGCTCACAGTGAGAGAAATTTTGCA 389  
QY 517 ACTTACGATTAATTAATGCTGCTGCTGATTAATGAAAGGACAAAGACGGGATTT 576  
Db 390 GCAATGAAGTTGTCTACTCAATGCAAAAGGATGATCTGATCTCTGAGAAATATGACAGTG 449  
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QY 637 TGAACATCAGCTTAAGTACGCTCAAGTACCAAGCAAGATGTACACAAAGACCTGCA 696  
Db 510 TATCTTATCAGCAGCAGCAGCATATTCCTACTACATCTTAGGCGCTCAACATTTG 569  
QY 697 TTGTCATGGGGTTTATGCTGTAATCTCTAACAAGTTTGTAGATTAATCTTGACG 756  
Db 570 TGTTAATGAACTCACTGACGACAGTCCCTTGATGATGATTTTCAAAAGATCGGAG 629  
QY 757 GTGACCATCTGCATATGAGCAGTACTTTGGAAGTGCAAAGGCTTTTGTAGCAGTATC 816  
Db 630 AAGACCTTCAATTTATTTGGCAGGTTTGGCAGGCCCTGACCTGATCTCATATTTATC 689  
QY 817 CGGGGATTAATGGGAACCATGAGA-----ATGAGTCATTTGCTTCGCTGACG 867  
Db 690 CAGCTTCAACCATGGTGTATATAGTAAAGCTCCAAATTAAGTTTATGATGATGAC 749  
QY 868 GGAACCGAAATGTTATCCAGCAGCAACTCTCCGAAAGACGTGTCATTTAGTTG 927  
Db 750 GCAGAAAGACATGTATCATCCAAAGAGCTGATCTCTTAAGACATGCTTATTCGTGG 809  
QY 928 AGCTGAGTGGAGCATGGAAGGACTCCGTCGATCATGCGCAAGCAACAGTCTCATCA 987  
Db 810 ATGTAGTGAAGTGTATGTAGTTGACACTTAACCTATCCGAACATCTGCTCCGAA 869  
QY 988 TTTTGGATACACTTGGGAGTATGATCTTCAACATTAATGCTTATATAGAGAGCTTC 1047  
Db 870 TGTAGAAACCTCTCAGATATGATTTTGTGAATGTAGCTTCAATTAACGCAATGCTC 929  
QY 1048 ACTATGTGCAACTTGCCTGATGGAATTTGTGCAAGCCGACAGCAAAAGAGC 1107  
Db 930 AGGATGTAAAGCTTTTTCAGCACC-----TTGTCCAAAGCAAAATGTAAGAAATAAAAAG 983  
QY 1108 ACTCAGGAGCATCTGCAACAATTTTCCCAAGAAATTTGATTTGATTTGATGATCCTC 1167  
Db 984 TGTGAAAGAGCGGTGAATTAATTCACAGCCAAAGAAATTAAGATTAAGAGGCT 1043  
QY 1168 TGAATGAGCCTTCAACATTTCTGATTTCAACACAGGAGCAAGAGATCTGCA 1227  
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QY 1228 GTAGGCCATATGCTCATTAATGATGGGCGGTGACACCTATGATTAATCTTTGCA 1287

US-08-223-305C-36  
Sequence 36, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIORITY APPLICATION DATA:

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: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/620,250
: FILING DATE: 30-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/482,384
: FILING DATE: 20-FEB-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/603,751
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: NO PCT/US89/01408
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/176,899
: FILING DATE: 04-APR-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 52516 (P519739)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619)238-0999
: TELEFAX: (619)238-0062
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 35...3289
: OTHER INFORMATION: Standard name "alpha2e"
: NAME/KEY: 5'UTR
: LOCATION: 1...34
: OTHER INFORMATION:
: NAME/KEY: 3'UTR
: LOCATION: 3290...3579
: OTHER INFORMATION:
: ?
: ?
: US-08-223-305C-36
:
: Query Match 3.5%; Score 130.6; DB 2; Length 3579;
: Best Local Similarity 46.4%; Pred. No. 8e-22;
: Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps
:
: Oy 346 AGAATACCAAGAGATGAGAAAGACGTTGCCATGAGAAATTTGATGGCTCCCACTGG 405
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: Db 270 TAGAATATTGCAGCCAGGGATATTGAGAAACTTCTAGCAGACAGATCTAAAGCCCTGGTGA 329
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: Db 330 GCCTTGCAATGGAAACCGGAGAAAGTTCAAGCAGCTCACCCAGTGAGAGAAAGATTTTGCCAA 389
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Db 510 TATCTTATACAGCAGCAGCATCCATATTTCTACTGATCTATGAGGGCTCAACATTTG 569  
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RESULT 9  
US-08-949-386-32  
Sequence 32, Application US/08949386  
Patent No. 6090623  
GENERAL INFORMATION:  
APPLICANT: Harpod, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: US  
ZIP: 92101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,386  
CLASSIFICATION:  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,012  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 08/149,097  
FILING DATE: 5-NOV-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/105,536  
FILING DATE: 11-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 519808  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 238-0999  
TELEFAX: (619) 238-0062  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 35..3289  
OTHER INFORMATION: /standard\_name="Alpha-2e"  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..34  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 3289..3579  
US-08-949-386-32

Query Match 3.5%; Score 130.6; DB 3; Length 3579;  
Best Local Similarity 46.4%; Pred. No. 8e-22;  
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;





Db 1335 TGGTTTACGAGGAGCAAGGTAAAGCAAGTCCAAATGAGCAATGTGTAACCTGATGCAT 1394  
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 Db 1635 CTCAGAGCGCA 1645

RESULT 11  
 US-08-984-709A-32  
 : Sequence 32, Application US/08984709A  
 : Patent No. 6320032  
 : GENERAL INFORMATION:  
 : APPLICANT: Williams, Mark E.  
 : APPLICANT: Stauderman, Kenneth A.  
 : APPLICANT: Harpold, Michael M.  
 : TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS; AND  
 : TITLE OF INVENTION: METHODS  
 : NUMBER OF SEQUENCES: 52  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESSEE: Heller Ehrman White & McCauliffe  
 : STREET: 4250 Executive Square, Suite 700  
 : CITY: La Jolla  
 : STATE: California  
 : COUNTRY: US  
 : ZIP: 92037  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FastSeq Version 1.5  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/984,709A  
 : FILING DATE: 02-DEC-1997  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Seidman, Stephanie L.  
 : REGISTRATION NUMBER: 33,779  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (619) 450-8400  
 : TELEFAX: (619) 587-5360  
 : INFORMATION FOR SEQ ID NO: 32:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 3579 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: DNA (genomic)  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: 35..3289  
 : OTHER INFORMATION: /standard\_name= "Alpha-2e"  
 : FEATURE:  
 : NAME/KEY: 5'UTR  
 : LOCATION: 1..34  
 : FEATURE:

NAME/KEY: 3'UTR  
 LOCATION: 3289..3579  
 US-08-984-709A-32  
 Query Match  
 Best Local Similarity 46.4%; Score 130.6; DB 4; Length 3579;  
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;  
 QY 346 AGAATATCAAGAGTATGAGAAAGACCTGGCCATAGAGAAATGATGGCTCCAACTGG 405  
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 Db 330 GCCTGGCATTGGAGCGGAGAAAGTTCAAGCAGCTCACCAGTGGAGAGAGATTTTGCA 389  
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 Db 450 ACCAGGAGCGCAGAGAGATTAAGAACTGTTTCTATTGAAGATCTTAATTTGGACGACAA 509  
 QY 637 TGAACATCAGTCTAAGTACGTCGCAAGTACCAAGACATGATACAAAGACCCCTGCA 696  
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 QY 697 TTGTCATAGGGGTTTATTTGCTGTAATCTTAACAAAGTTTGTATGATACTTTGAC 756  
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 QY 1168 TGAATGAGCCTTCAACATTTGAGTATTTCAACCAAGGAGCAAGAGATATCTGCA 1227  
 Db 1044 TTAGTTTGTCTTTTGAACAGCTCTTAATTAATATGTTTCCAGACA-----ACTGCA 1097  
 QY 1228 GTCAGGCCATCATCTCATTAAGTATGAGGCGGTGACACCACTATGATATCAATCTTGGCA 1287  
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 QY 1288 AATACAAATTGGCCAGATCCAGAAAGTTGCACTTCACTATCTCATTTGAGAGAGGCTG 1347

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1215 ATGAGACAGACCTATTCAGTGGATGCGCTGTGAAACAAAGTTATATATGAAATTC 1274  
1408 CCACTTGGCTGATGTCAGAGATGTCATGCAATACCTTCAGTGTGATGCGGCCCA 1467  
1275 CTTCATTTGGTCAATTAAGATCAATCTCAGCAATTTTGGATGTTTGGAGACCAA 1334  
1468 AAGTCAT-----CGACCAGAGCATGATGTTGTTGACCGAAGCTTACATGACACA 1521  
1335 TGGTTTACGAGGACAAAGCTAAGCAAGTCAATGACAAATGTACTGATGATCAT 1394  
1522 CTCTGATGATGATGACAGGCGCCCTCTGTGACCACTGATGACCATGCTGTGTTAGTA 1561  
1395 TGGAACTGGAGCTTGTCTTACTGGAACCTCTCGCTTCAACATTAACCGCCAAATTTG 1454  
1582 AGCAAGACGAACACGATCGAGGCGCATCTCTGGAGTGGTGGACAGATGCTCCAG 1641  
1455 AATAATAGCAAACTTAAGAACACAGTGTCTTGTGTGATGGAGTGAATGTCTT 1514  
1642 TGAAGAACTTGAAGACCATCCCAATATCAAGTTAGGATTCACGTTATGCTTTG 1701  
1515 TGGAGATATTTAAAGACTGACACACAGTTTACACTGTGCCCAATGGTATTACTTTG 1574  
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RESULT 12  
US-08-450-272-32

Sequence 32, Application us/08450272  
Patent No. 6387696

GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: McCue, Ann  
APPLICANT: Gillespie, Allison  
APPLICANT: Feldman, Daniel  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: US  
ZIP: 92101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450.272  
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/404,950

FILING DATE: 13-MAR-1995

APPLICATION NUMBER: 08/336,257

FILING DATE: 7-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/314,083  
FILING DATE: 28-SEPT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/311,363  
FILING DATE: 23-SEPT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/290,012  
FILING DATE: 11-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: 4-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/193,078  
FILING DATE: 07-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/149,097  
FILING DATE: 5-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/105,536  
FILING DATE: 11-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/914,231  
FILING DATE: 13-JULY-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: 10-APR-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06903  
FILING DATE: 14-AUG-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/745,206  
FILING DATE: 15-AUG-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-519812  
TELEPHONE: (619) 238-0999  
TELEFAX: (619) 238-0062  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 35..3289  
OTHER INFORMATION: /standard\_name="Alpha-2e"  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..34  
FEATURE:  
NAME/KEY: 3'UTR  
LOCATION: 3289..3579  
US-08-450-272-32

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Best Local Similarity 3.58; Score 130.6; DB 4; Length 3579;

Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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210 ATATTATGAGAAATATCAACATTTGTATCTGTGGAACCAATATATGACGCGCAGCTGG 269





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APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name= "Alpha-2"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-455-543A-11

Query Match      3.5%; Score 130.6; DB 1: Length 3600;
Best Local Similarity 46.4%; Pred. No. 8e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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DB 750 GCAGAGACCATGCTACATCCAGAGCTGATCTCTTAAGACATGCTTATTTCTGTGG 809
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DB 1635 CTCAGGAGCA 1645
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RESULT 14
US-08-455-543A-33
Sequence 33 Application US/0845543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: Mccue, Ann
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Db 1275 CTTGCATTTGGGCAATAGATCAATCACTACTGAGCAATATTTGGATGTTTGGAGACCA 1334
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Db 1635 CTCGAGAGCA 1645

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RESULT 15
US-08-193-078B-11
Sequence 11, Application US/08193078B
Patent No. 5846757
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
STREET: 1660 UNION STREET
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
FAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

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LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name="Alpha-2b"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
NAME/KEY: 3'UTR
LOCATION: 3308..3600
US-08-193-078B-11
Query Match 3.58; Score 130.6; DB 2; Length 3600;
Best Local Similarity 46.48; Pred. No. 8e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
QY 346 AGAATACAAAGATGATGAGAAAGAGCTGCAATAGAAAGAAATTTGGCTCCACTGG 405
Db 210 ATATTATGAGAAATATCAAGATTTGTATCTGTGGAACCAATTAATGACGCCAGCTGG 269
QY 406 TAAAGAGCTGGCAAGAACATGAGAGATGTTTCACAAGAGTCTGAGCCGTCAGGC 465
Db 270 TAGAAATTCAGCAGCAGGATATTGAGAACTTCTGACCAACATCATTAAGCCCTGTGA 329
QY 466 GTCTG-----GTGGAGGCTGCAAGACACACCTGAAACATGAATTTGATGACAG 516
Db 330 GCCTGGCATTGGAAGCGGAGAAAGTTCAACACCTCACCAGTGGAGAGAAATTTGCAA 389
QY 517 ACTTACGATGAATCTCAATCTGCTGTGATTAATGAAGGCAAGAGGCAATTT 576
Db 390 GCAATGAGTGTCTACTACAAATGCAAGATATCTCGTCTGTGAAATTAATGACAGTG 449
QY 577 TTTTGGAGCTGGGAAAGAAATTCATCTTACCCCAATGACATTTTAATTTCCCTG 636
Db 450 AGCCAGCAGCCAGAGAGATTAACCTGTTTCAATGAAGATGCTAATTTTGGACGACAA 509
QY 637 TGAACATCACTTAAGTACAGTCAAGTACCAAGCAACATGTACAAAGAACCTCGCA 696
Db 510 TATCTTATGACGACGAGAGATTCATATTCCTGACATCATATGAGGGCTCAACATTTG 569
QY 697 TTGTCAATGGGGTTTATGCTGATCTCTTAACAAAGTTTGTGATTAATCTTTGAC 756
Db 570 TGTTAATGACTCACTGACAGATGCTTATGATGAAGTTTCAAAAAGAAATTCGGAGG 629
QY 757 GTGACCCATCTCATATGAGAGTACTTTGGAAGTCAAGGAGCTTTTATAGCAGTATC 816
Db 630 AAGACCTTCATATATGTGCAAGTTTTGGCAGTCCCACTGCGCTGATCATATATAC 689
QY 817 CCGGATTTAAATGGGACCAAGTGA-----ATGGAATCATTTGCTTCACTGCA 867
Db 690 CAGCTTCAACATGGTGTGTAATAGTAACCTCAAAATGAATGACCTTTATGATGTAC 749
QY 868 GGAACGAAATGTGATCATGACGAGCAACCTTCCGAAAGAGCTGGATTTATGTTG 927
Db 750 GCAGAAAGACATGATACATCCAGAGGCTGCAATCTTAAGACATGCTTATTTGGTGG 809
QY 928 AGCTAGTGGAGCATGAAAGAGCTCCGCTGACTGATGCGCAAGCAAGACGCTCATCA 987
Db 810 ATGTGATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 869
QY 988 TTTTGGATCACTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047
Db 870 TGTGAAAGACCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 929
QY 1048 ACTATGGAACCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107
Db 930 AGGATGTAAAGCTTTTTCAGAC-----TTGTCCAAAGCAAAATGTAAGAAATAAAG 983

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QY 1108 ACTTCAGGAGCATCTGGACAACTTTTCGCCAAGGAATGGATGTGATATAGCTC 1167  
1167 TGTGAAAGACGGGTGAATATATACACAGCAAGGAATTTACAGATTTAAGAGGGCT 1043  
QY 1168 TGAATGAGGCTTCACATCTGTGATGATTTCAACCCACGCGGCAAGGAATATCTGCA 1227  
1044 TTATGTTTGGTTTGAACACCTGCTTAATATATATGTTTCCAGAGCA-----AACTGCA 1097  
QY 1228 GTCAGGCCATCATCATTAATGATGGGGGGTGGACACCTATGATATACATCTTTGCAA 1287  
1098 ATAGATTTATATGCTATTCACGATGGAGAGAAAGAGAGCCACGAGATATTTAACA 1157  
QY 1288 AATACATTTGGCCAGATCGAAAGGTTGCAATCTTCATCTCATTTGACGAGAGGCTG 1347  
1158 AATACATTT-----AAAGATTAATAAGTACGTGATTTCAAGTTTTCAGTTGTCACACATTT 1214  
QY 1348 CGTTTCAGACATCTAATGATGATGGCTGTGTCACCAAGAGATTTTTCACCAAGATCT 1407  
1215 ATGAGAGAGAGACCTATTCAGTGGATGGCTGTGMAAAACAAAGTTATTTATGAATTC 1274  
QY 1408 CCACCTTGGCTGTGTCAGAGAAATGTCATGATACCTTCACGTGCTTAGCGGCGCA 1467  
1275 CTTCATTTGGTGAATTAATCAATACACAGAAATATTTGGATGTTTGGAGAGACCA 1334  
QY 1468 AAGTCTT-----CGACCAAGAGCATGATGTGTGTGACCGAAGCTTACATTCACAGCA 1521  
1335 TGGTTTTACAGAGAGCAAAAGCTAAGCAAGTCCAAATGACAAATGTACCTGATGCAAT 1394  
QY 1522 CTCTGACATGATGACGGGCCCCGCTCTGATGACCACTGTAGCCATGCTGTGTTAGTA 1581  
1395 TGGAACTGGACTTGTATTAATGAACTTTCGGTCTTCAACATPACCGCCCAATTTG 1454  
QY 1582 AGCAGAACGNAACAGATGCAAGGCAATCTTCTGGAGTGGTGGACAGATGTCCAG 1641  
1455 AAAATAAGCAAACTTAAGAACCAAGCTGATCTTGTGTGATGGAGTAGATGTCTT 1514  
QY 1642 TGAAGAAGCTTCTGAAGACCATCCCAATACAGTTAGGATTCACGTTATGCCCTTG 1701  
1515 TGGAGATATTTAAAGACTGACACACGTTTACACTGTGCCCAATGSGTATTAATTG 1574  
QY 1702 CAATCACAATTAATGSRATATCCCTGAGCGATCCGGAATCTCAGGCTGCTGTACGAAGAG 1761  
1575 CAATGATCTTAATGTTATGTTTATTAATCAATCTTCAGCCAAAGAAACCCCAAT 1634  
QY 1762 GAAAAAAGCGA 1772  
1635 CTCAGAGAGCA 1645  
Db

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